

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:25:46 ; Search time 19 Seconds

(without alignments)
1189.031 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242

Sequence: 1 MVLAPAMSPPTLYLLLL...RCGEVPPVPSQDLVLRH 235

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

PIR_73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	2	138440
2	864.5	69.6	245	2	543293
3	834	67.1	178	2	139076
4	768.5	61.9	231	2	A49265
5	606.5	48.8	220	2	543291
6	606.5	48.8	220	2	158343
7	93	7.5	1217	2	T22672
8	92	7.4	661	1	TNBE12
9	89.5	7.2	474	2	T19543
10	89	7.2	387	2	148201
11	89	7.2	793	2	148201
12	88.5	7.1	238	2	AB1990
13	88.5	7.1	1386	2	T00257
14	88	7.1	753	2	T00257
15	87.5	7.0	479	1	A32250
16	87	7.0	910	2	A53137
17	86.5	6.9	590	2	A40437
18	86	6.9	299	2	T17832
19	86	6.9	485	2	A33647
20	86	6.9	746	2	T28004
21	85	6.8	289	2	A87646
22	85	6.8	366	2	A37374
23	84	6.8	263	2	T03162
24	84	6.8	757	2	A39283
25	83.5	6.7	189	2	E75630
26	83.5	6.7	530	2	A45650
27	83	6.7	1509	2	T19486
28	82.5	6.6	418	2	T19800
29	82.5	6.6	426	2	136948

ALIGNMENTS

30	82.5	6.6	512	2	D40829	activin receptor 1
31	82.5	6.6	513	2	J01484	activin receptor p
32	82	6.6	106	2	T06479	proline/leucine-ri
33	82	6.6	854	2	T23837	hypothetical prote
34	81.5	6.6	485	2	C73460	hypothetical prote
35	81.5	6.6	488	2	S13423	stromelysin 3 (EC
36	81.5	6.6	958	2	T13593	hypothetical prote
37	81.5	6.6	1119	2	T50995	related to cytoske
38	81	6.5	196	2	B48232	cysteine-rich exte
39	81	6.5	209	2	A48332	hypothetical prote
40	81	6.5	294	2	A12016	probable transpos
41	81	6.5	388	2	S15591	class I cytokinase
42	81	6.5	428	1	EHU	hypothetical prote
43	80.5	6.5	636	2	JM0047	hypothetical prote
44	80.5	6.5	1176	2	T49482	hypothetical prote
45	80.5	6.5	1306	2	T13592	hypothetical prote

RESULT 1

I38440

flr3 ligand - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #extl_change 01-Dec-2000

C:Accession: I38440; 139075; 543292

R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe

Blood 83, 2795-2801, 1994

A>Title: Cloning of the human homologue of the murine flr3 ligand: a growth factor fo

A:Reference number: I38440; MUID:94235842; PMID:8180375

A:Accession: I38440

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-235 <RES>

A:Cross-references: EMBL:029874; NID:9494978; PIDN:AAA19825.1; PID:9494979

R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.

Oncogene 11, 1165-1172, 1995

A>Title: Structural analysis of human and murine flr3 ligand genomic loci.

A:Reference number: 139075; MUID:96032581; PMID:7566577

A:Accession: 139075

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-235 <RES>

A:Cross-references: EMBL:029874; NID:9494978; PIDN:AAA0949.1; PID:91072037

R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Baran, J.F.;

Mature 368, 643-648, 1994

A>Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopo

A:Reference number: S43290; MUID:94195428; PMID:8145851

A:Accession: S43290

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-71, 'A', '73-235 <HAN>

A:Cross-references: GB:004806; NID:9483844; PIDN:AAA17999.1; PID:9483845

A>Note: The authors translated the codon AGT for residue 25 as Met

C:Genetics:

A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3

Query Match 100.0%; Score 1242; DB 2; Length 235;

Best Local Similarity 100.0%; Pred. No. 5, 4e-99;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MVLAPAMSPPTLYLLLLSSGSGTDCSROHSPISDFVAKTRELSDYLLDYPYTV 60

DB 1 MVLAPAMSPPTLYLLLLSSGSGTDCSROHSPISDFVAKTRELSDYLLDYPYTV 60

OY 61 ASNLODEELCGIMRVLVAQRMERLKTVAAGSKMGLERVTETHTFKCAFOPPPSCL 120

DB 61 ASNLODEELCGIMRVLVAQRMERLKTVAAGSKMGLERVTETHTFKCAFOPPPSCL 120

OY 121 REVQINISRLLOETSEQVIAKPMWITRONFSRCLQLACQOPSSSTLPWSPPLPPLATAPY 180

Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELOCOPDSSITLPPWSPRIEATAPT 180
 QY 181 APOPLLILLLLPVGLLLAAAMCLHMQRTRRRTPRGEQVPVPSDOLLVH 235
 Db 181 APOPLLILLLLPVGLLLAAAMCLHMQRTRRRTPRGEQVPVPSDOLLVH 235

RESULT 2

S43293
 FLT3/FLK2 ligand (clone S109) - human
 C:Species: Homo sapiens (man)
 C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
 C:Accession: S43293
 R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kelf, A.; Muench, M.; Kellner, G.; Nankikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A. Nature 368, 643-648, 1994
 A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of hematopoietic
 A:Reference number: S43290; MUID:94195428; PMID:8145851
 A:Accession: S43293
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-245 <HNA>
 A:Note: the authors translated the codon AGC for residue 25 as Met

Query Match 69.6%; Score 864.5; DB 2; Length 245;
 Best Local Similarity 73.0%; Pred. No. 1.2e-66;
 Matches 176; Conservative 7; Mismatches 27; Indels 31; Gaps 3;

QY 1 MYLAPAMSPITYLLILLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYVTV 60
 Db 1 MYLAPAMSPITYLLILLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYVTV 60
 QY 61 ASNLODEELCGGLMRVLVAORMERLKTVAAGSKMOGLLEVNTEIHFVTKCAFOPPSCL 120
 Db 61 ASNLODEELCGGLMRVLVAORMERLKTVAAGSKMOGLLEVNTEIHFVTKCAFOPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELOCOPDSSITLPPWSPRIEATAPT 180
 Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELOCOPDSSITLPPWSPRIEATAPT 180
 QY 181 APOPLLILLLLPVGLLLAAAMCLHMQRTRRRTPRGEQVPVPSDOLLVH 235
 Db 181 APOPLLILLLLPVGLLLAAAMCLHMQRTRRRTPRGEQVPVPSDOLLVH 235
 QY 228 Q 228
 Db 223 E 223

RESULT 3

FLT3 ligand alternatively spliced isoform - human
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
 C:Accession: I39076
 R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S. Oncogene 11, 1165-1172, 1995
 A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
 A:Reference number: I39075; MUID:96032581; PMID:7565977
 A:Accession: I39076
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-178 <RES>
 A:Cross-References: EMBL:U29874; NID:91072036; PIDN:AAA90950.1; PID:91072038
 C:Genetics:
 A:introns: 11/3; 48/3; 66/3; 114/3; 161/1

Query Match 67.1%; Score 834; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 3.3e-64;
 Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MYLAPAMSPITYLLILLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYVTV 60
 Db 1 MYLAPAMSPITYLLILLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYVTV 60

Db 1 MYLAPAMSPITYLLILLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYVTV 60
 QY 61 ASNLODEELCGGLMRVLVAORMERLKTVAAGSKMOGLLEVNTEIHFVTKCAFOPPSCL 120
 Db 61 ASNLODEELCGGLMRVLVAORMERLKTVAAGSKMOGLLEVNTEIHFVTKCAFOPPSCL 120

QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELOCOP 160
 Db 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLELOCOP 160

RESULT 4

A49265
 FLT3/FLK-2 ligand precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
 C:Accession: A49265; I49347; I49346; S43290
 R:Lyman, S.D.; James, L.; Vanden Bos, T.; de Vries, P.; Brasel, K.; Gliniak, B.; Holl Cell 75, 1157-1167, 1993
 A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor:
 A:Reference number: A49265; MUID:94084791; PMID:7505204
 A:Accession: A49265
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-231 <LYM>

A:Cross-References: GB:U23636; NID:9439441; PIDN:AAA9436.1; PID:9439442
 R:Lyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S. Oncogene 11, 1165-1172, 1995
 A:Title: Structural analysis of human and murine flt3 ligand genomic loci.
 A:Reference number: I39075; MUID:96032581; PMID:7565977
 A:Accession: I49347
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-163; 'G', 165, 'HYAG' <RES>

A:Cross-References: EMBL:U29875; NID:91072039; PIDN:AAA90952.1; PID:91072041
 A:Accession: I49346
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-197; 'L', 198-231 <RES>

A:Cross-References: EMBL:U29875; NID:91072039; PIDN:AAA90951.1; PID:91072040
 R:Hanum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kelf, A.; Muench, M.; Kellner, G.; Nankikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik Nature 368, 643-648, 1994
 A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoi
 A:Reference number: S43290; MUID:94195428; PMID:8145851
 A:Accession: S43290
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-197; 'L', 198-231 <HNA>

A:Residues: 1-197; 'L', 198-231 <HNA>
 A:Experimental source: clone T110
 A:Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-
 C:Genetics:
 A:introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3
 C:Keywords: transmembrane protein

Query Match 61.9%; Score 768.5; DB 2; Length 231;
 Best Local Similarity 70.3%; Pred. No. 1.8e-58;
 Matches 163; Conservative 17; Mismatches 43; Indels 9; Gaps 4;

QY 1 MYLAPAMSPITYLLILLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYVTV 59
 Db 1 MYLAPAMSPNSLILLLLPCLRTGTPCYFSHPISSNFVKFRELTDHLKDYPTV 60
 QY 60 VASNLODEELCGGLMRVLVAORMERLKTVAAGSKMOGLLEVNTEIHFVTKCAFOPPSCL 119
 Db 61 VASNLODEELCGGLMRVLVAORMERLKTVAAGSKMOGLLEVNTEIHFVTKCAFOPPSCL 120
 QY 120 LRFVQTNISRLQETSEQLVALKPWITR--QNFSCLELOCOPDSSITLPPWSPRIEAT 177
 Db 121 LRFVQTNISRLQETSEQLVALKPWITR--QNFSCLELOCOPDSSITLPPWSPRIEAT 180
 QY 178 APTAPPP--LLLLLPVGLLLAAAMCLHMQRTRRRTPRGEQVPVPS 227

QY 124 QTNISRLQETSEOLVAKPWITRONFSRCLELOCQDDSTLPPMSP-RPLEATAPAP 182
 Db 198 NSDYRGICQELREALGAVQKYM---YFMR-----PDDPTNPSPDRIRFVQETIAAYAT 247
 QY 183 QPRLILLLLPVGILLAAAMCWMORTRRTPRGSEVPVPSPDIL 231
 Db 248 GYGMMLFLVDVDD---ARVCRHLKLOFRIRINGPRASV---IPDDL 287

RESULT 9

T19543
 hypothetical protein C28D4.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C/Accession: T19543
 R/Murray, A.
 submitted to the EMBL Data Library, November 1996

A/Reference number: 219139
 A/Accession: T19543
 A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA
 A/Residues: 1-474 <MIL>
 A/Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2

C/Genetics:
 A:Experimental source: clone C28D4
 A:Gene: CESP:C28D4.2
 A:Map position: 4
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Query Match 7.2%; Score 89.5; DB 2; Length 474;
 Best Local Similarity 24.1%; Pred. No. 5.5;
 Matches 59; Conservative 29; Mismatches 82; Indels 75; Gaps 15;

QY 27 TQDC-----SFQHS-PISSDFAVKIREL-SDYLLQDYPTVANSILODELGGIMRL 76
 Db 65 TTDCVDLKKVFSKFDSSAPISGEILFRFLCAKYL-----GGAARK 106
 QY 77 VLAQRMMERLKYAGSMQGLERVENIEHFVKCAQPPBSCLR-FVQTNISRLQET- 134
 Db 107 VKIEEF--RIRATGG-MSMLFLVELPAH-LPIQMEPRKALRVHCOSIDIDLLSESV 162
 QY 135 -----SEOLVAKPWITRONFSRCLELOC-----QDDSTLPPMSPR-PLEATA 178
 Db 163 VFTLISRNIGPKMLGFFPGREGQFIPSRALOCLEISKGLSLIPIYARVHTLDAPL 222
 QY 179 PTAPQPLILLLLPVGLLLAAAMCLMORTRRTP--RPGE-----QVPVPSPD 229
 Db 223 PKREQ-----TLQTAQMLERF-----KKMPAGSRPTIMYLTQAKVPSDYPT 266
 QY 230 LLAVE 234
 Db 267 ITVAQ 271

RESULT 10

I48201
 adhalin - golden hamster

C/Species: Mesocricetus auratus (golden hamster)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Jun-2000
 C/Accession: I48201
 R/Roberts, S.L.; Campbell, K.P.
 FEBS Lett. 364; 245-249, 1995

A/Title: Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic hamster.
 A/Reference number: I48201; MUID:95278335; PMID:7758576
 A/Accession: I48201

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA

A/Residues: 1-387 <RES>
 A/Cross-references: EMBL:U21677; NID:9726481; PIDN:AAA81645.1; PID:9726482

C/Superfamily: mouse adhalin

Query Match 7.2%; Score 89; DB 2; Length 387;
 Best Local Similarity 23.4%; Pred. No. 4.8;

Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

QY 11 TTYILLILLSSGTCDDCSFHSPISDPAVKIRELSDYLLQDYPTVANSILODEELC 70
 Db 115 TTRORLLILLI-----BDPEGRLPYQAEFLVRSADVVEVL---PSTPANRL-TAL 161
 QY 71 GGLMRL-----VLAQRMMERLKYAGSMQGLERVENIEHFVT-----K 110
 Db 162 GGLMELGELQOLLNITSALDRGRVPLPIEGKREGVYIKVGSATPTSTCLKVAPSDYAR 221
 QY 111 CAFQPPP--SC-----LRFVQTNISRLQETSEOLVAKPWITRONFSRCLELOCOPD 161
 Db 222 CAQCGPPLLSQCYDSLAPHFVDMCVSLVSKSVPEPLD-----EVPFGD 266
 QY 162 SSTLPPMSPRPLEAT-----APTAPQPLILLLLPVGILLAAAMC----- 204
 Db 267 GILHDFPCPTTEATGDFLADALVTLVPLVALL--TLLAYIMCCRRGECOLKRD 323
 QY 205 -----LHWQTRRRTRTP-----GEQVPP-VPSPQ-DLL 231
 Db 324 MATSDIQVHHCTHGNTEELROMAAREVRPLSTLPMFNVRIGERLPPRVDASQVPLI 383
 QY 232 LVEH 235
 Db 384 LDQH 387

RESULT 11

S60735
 splicing factor SF3a 120K chain - human

C/Species: Homo sapiens (man)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C/Accession: S60735; S60733
 R/Kraemer, A.; Mulhauser, F.; Wersig, C.; Groening, K.; Blube, G.
 RNA 1; 260-272, 1995

A/Title: Mammalian splicing factor SF3a120 represents a new member of the SURP family
 A/Reference number: S60733; MUID:96079958; PMID:7489498
 A/Accession: S60735
 A/Status: nucleic acid sequence not shown

A/Molecule type: mRNA
 A/Residues: 1-793 <KRA>

A/Cross-references: EMBL:X85237; NID:9899297; PIDN:CAA59494.1; PID:9899298
 A/Accession: S60733
 A/Molecule type: protein

A/Residues: 51-62; 82-94; 270-275; 397-414; 448-463 <KRA>
 A/Genetics:
 A:Gene: GDB:SF3A120; PRP21; SAP114
 A/Cross-references: GDB:9955873

A/Map position: 22q12.1-22qter
 C/Superfamily: human splicing factor SF3a 120K chain; ubiquitin homology
 C/Keywords: pre-mRNA splicing
 F:714-790/Domain: ubiquitin homology <UBH>

Query Match 7.2%; Score 89; DB 1; Length 793;
 Best Local Similarity 22.3%; Pred. No. 11;
 Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

QY 4 LAPMSPTTYILLILLSSGTCDDCSFHSPISDPAVKIRELSDYLLQDYPTVANS 63
 Db 401 LPPAPAPDEVLY-----SPITGE--KI-----PAK 424
 QY 64 LQDELGCGMLRVLAQRME-RLKTV-----ASCKMGLERVENTIHF 107
 Db 425 MQEHRIG-----LLDRPMLQGRDRSIREKOSDDEVYAPGLDISSIKQLNER-RTDIFG 478
 QY 108 VTKA-----FQPPSCLRF-----VQTNISRLQETSEOLVAKPWIT 145
 Db 479 VEETAIAKKIGEEIQRPEEKVTWDGSHGSMARTQAQANIT--LOEITAIHKAKGLV 536
 QY 146 -----TRONF--SRCLELOCOP-----DSTLTP-----PWSRPLEAT-----APT 180
 Db 537 PEDDTKEIKGSKNEIIPQDPPPSATINIPSSAPPIITSVPRPTMPBPVATTYVSAVP 596

OY 181 APQPLLLLLPVGLLLAAACLMWORTR-----RTPRRGEVPP---VPSP 227
 Db 597 MRPMMASVRLRPPGSLVAPMPPIIHAPRINVPMPSPAPRPMAPRPPMIVTAPVAP 656

RESULT 12

AB1990
 hypothetical protein all1471 (imported) - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp.
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
 C:Accession: AB1990
 R:Kanehiko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irituguhi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AB1990
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-238 <KUR>
 A:Cross-references: GB:BA000019; PIDN:BA877837.1; PID:g17135292; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all1471

Query Match 7.1%; Score 88.5; DB 2; Length 238;
 Best Local Similarity 20.8%; Pred. No. 3;
 Matches 44; Conservative 32; Mismatches 59; Indels 77; Gaps 9;

OY 34 HSPISDFAVIRRELDYLDY---PYTVASNLDDDELGLMLRYLQRMWERTKTA 90
 Db 84 HSKTITTYESINEYCNQYLKSYKKPLVIT-----QLG--W---SQRIMRYKTYD 131
 OY 91 GSKMOGLIERVNTIEHVTKCAFPDPSCLEFVQTNISRLD-----ETSEQ 137
 Db 132 DDDTDIDISPGISTEV-----VVRKIPRIVETPRIVKQKTEDITLES 174
 OY 138 LVAKPWITRQNFSCLELQCPDSTLPPV---SPRLENTAPAPOPPLLLLLLV 194
 Db 175 POSLKP--TKPIPPLEPKSEDSKNLQRPRIIPSPKIKNSOEPAPV----- 223
 OY 195 GLLLAAACLMWORTRRTRPRGQVPPVS 226
 Db 224 -----EPPKPMERVKKPS 237

RESULT 13

T00257
 hypothetical protein KIAA0476 - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 24-Jul-2000
 C:Accession: T00257
 R:Seiki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
 DNA Res. 4, 345-349, 1997
 A:Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human
 A:Reference number: Z14085; MUID:98116662; PMID:9455484
 A:Accession: T00257
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1386 <SEK>
 A:Cross-references: EMBL:AB007945; NID:g3413913; PIDN:BA432321.1; PID:g3413914
 A:Experimental source: Brain
 C:Genetics:
 A:Note: KIAA0476

Query Match 7.1%; Score 88.5; DB 2; Length 1386;
 Best Local Similarity 23.1%; Pred. No. 23;
 Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;

OY 21 SSGISGTCDFQHSFSDFAVIRRELDYLDYPTVANSNLDDDEL---GGLMRL 76
 Db 1104 SAGASGSKDAVPVPGP-----GVLSDRRLCLA--LDEPOLCNGHMGASRR 1148

OY 77 VLAQRMRERKTVAGSKMOGLIERVNTIEHVTKCAFPDPSCLEFVQTNISRLDQTS 136
 Db 1149 VESGAMAYLSPLVLRKLESLVENEGSEV-----LALPELPSAHPIIFWMLNTRFQL-- 1201
 OY 137 QLVAKPWITRQNFSCLELQCPDSTLPPV---SPRLENTAPAPOPPLLLLLLV 185
 Db 1202 RLPSILPLGLVLAS-----CGPSSHQCAPSPWLPDPASVQVRLMDVLTDPDNCSP 1253
 OY 186 LLLLLLPVGLLLAAACLMWORTRRTRPRGQVPPVSPODLLVE 234
 Db 1254 LTVL-----WRVHSQ--IPQVVPVPG---PVPASLSLALLE 1284

RESULT 14

J00532
 OP protein - Kennedy yellow mosaic virus
 C:Species: Kennedy yellow mosaic virus
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999
 C:Accession: J00532
 R:Ding, S.; Keese, P.; Gibbs, A.
 J. Gen. Virol. 71, 925-931, 1990
 A:Title: The nucleotide sequence of the genomic RNA of Kennedy yellow mosaic tymovir
 A:Reference number: J00532; MUID:90218040; PMID:2324710
 A:Accession: J00532
 A:Molecule type: mRNA
 A:Residues: 1-753 <DIN>
 A:Cross-references: GB:D00637; NID:g221969; PIDN:BA400531.1; PID:d1000986; PID:g22197
 A:Experimental source: strain Jervis Bay isolate

Query Match 7.1%; Score 88; DB 2; Length 753;
 Best Local Similarity 22.3%; Pred. No. 12;
 Matches 41; Conservative 19; Mismatches 58; Indels 66; Gaps 7;

OY 100 RVNTEIHFVTKCAFPDPSCLEFVQTNIS-----RLQETSEGLVAKWITR 147
 Db 420 RUSTOPPSSPQYSSPPSPRTDASGIQTPPLASPSKREKSLPPSHQ---PPSHK 475
 OY 148 ONFSR-----CLELQCPDSTLPPVSPRLENTAPAPOPPLLLLLLV 193
 Db 476 RNLRRSALPLPLPIHPTKTQHPRAVPO--TAGTTPRPPTKTLPLNPKSQERNPS 533
 OY 194 -----VGLLLAAACLMWORTRRTRPRGQVPPVS 226
 Db 534 PPDVFHDCQPSPTSHVGVYRLLGSGISLPFLAEW-----RRSRNPAHNLPRPP 586
 OY 227 PQDL 230
 Db 587 PKRL 590

RESULT 15

A32290
 Protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25 homolog string - fruit fly (Drosophila)
 C:Species: Drosophila melanogaster
 C:Date: 05-Oct-1989 #sequence_revision 25-Apr-1997 #text_change 11-Jun-1999
 C:Accession: A32290; S12008
 R:Edgar, B.A.; O'Farrell, P.H.
 Cell 57, 177-187, 1989
 A:Title: Genetic control of cell division patterns in the Drosophila embryo.
 A:Reference number: A32290; MUID:89195217; PMID:2702688
 A:Accession: A32290
 A:Molecule type: mRNA
 A:Residues: 1-479 <EDG>
 A:Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; PID:g158508
 R:Jimenez, J.; Alpay, L.; Nurse, P.; Glover, D.M.
 EMBO J. 9, 3565-3571, 1990
 A:Title: Complementation of fission yeast cdc2(ts) and cdc25(ts) mutants identifies t
 A:Reference number: S12008; MUID:91006056; PMID:2120044
 A:Accession: S12008
 A:Molecule type: mRNA
 A:Residues: 1-227; A', 229-479 <JIM>
 A:Cross-references: EMBL:X57495; NID:g7706; PIDN:CAA40732.1; PID:g7707

C:Genetics:

A:Gene: FlyBase:stg

A:Cross-references: FlyBase:FBgn0003525

C:Function:

A:Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and

A:Note: cdc25 activates the cdc2 protein kinase by dephosphorylating it

C:Superfamily: protein-tyrosine-phosphatase string; cdc25-type protein-tyrosine-phosphat

C:Keywords: cell cycle control; mitosis; phosphoprotein; phosphoric monoester hydrolase;

F:352-456/Domain: cdc25-type protein-tyrosine-phosphatase homology <ppp>

F:379/Active site: Cys (phosphocysteine intermediate) #status predicted

F:385/Binding site: substrate phosphate (Arg) #status predicted

Query Match:

Best Local Similarity 7.0%; Score 87.5; DB 1; Length 479;

Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;

QY 1 MTVLAPAMSPFTYILL---LLLSGSLGTQDCSFOHSPISSDPAVKIRELSDTLLQDYP 57
 DB 72 MGLSPGSGPQRFOIVKPKILPAMGVSS-----DHTPARS-FRI-FNSLS- -T 117
 QY 58 VTVASNLQDELGGLWRLVLAQRMERLKTVAGSKMOGLLERVNTLHFVTKCAFQPP 117
 DB 118 CSMSSMWDE-----YMLFEMESQS-----QTALGF-----P 146
 QY 118 SCARFVQTNISRLQETSEQLVAKP---WITQNSRCLL-OCOPDSSTLPPWSPRP 173
 DB 147 SGLN-----SLISGQIKKEQPAKSPAGLSMRPVSVRCLSMTESNTNSTTTPPKTPE- 199
 QY 174 LEATAPTA---POPILLLLLLPVGILLAAAWCLHWQRTRRRTPRRGEOVPPVPSQDL 230
 DB 200 ---TANCCFRRPFP-----ASANCSPIQSKRHRCAVKEKENCAPPSPLSQ 242
 QY 231 LLYEH 235
 DB 243 VTISH 247

Search completed: May 27, 2003, 18:27:59
 Job time : 22 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:25:26 ; Search time 11 Seconds
(without alignments)

886.085 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242
Sequence: 1 MTVLAPAMSPFTYLLLL.....RPGQVPPVPSODLLVEH 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1242	100.0	235 1 FLJ3L_HUMAN	P49771 homo sapien
2	768	61.8	232 1 FLJ3L_MOUSE	P49772 mus musculu
3	92	7.4	661 1 ARI2_VZVD	P09264 varicella-z
4	89.5	7.2	941 1 GBR2_HUMAN	O75899 homo sapien
5	89	7.2	387 1 SGCA_MESAU	O64255 mesocricetu
6	89	7.2	793 1 S3AL_HUMAN	O15459 homo sapien
7	87.5	7.0	415 1 TNR3_MOUSE	P50284 mus musculu
8	87.5	7.0	479 1 WPIP_DROME	P20483 drosophila
9	87	7.0	910 1 DDRI1_RAT	O63474 rattus norv
10	87	7.0	911 1 DDRI1_MOUSE	O03146 mus musculu
11	86.5	6.9	1394 1 CNG4_BOVIN	O28181 bos taurus
12	86	6.9	485 1 SSGP_VOLCA	P21997 volvox cart
13	85	6.8	282 1 ARF5_HUMAN	O972d1 homo sapien
14	85	6.8	366 1 FCCN_RAT	P13599 rattus norv
15	84.5	6.8	3726 1 ABE1_MOUSE	O61329 mus musculu
16	84	6.8	582 1 MNT_HUMAN	O09583 homo sapien
17	84	6.8	732 1 YF48_HUMAN	O9hcm4 homo sapien
18	84	6.8	1234 1 NPHN_RAT	O9r444 rattus norv
19	83.5	6.7	671 1 Z282_HUMAN	O9uav7 homo sapien
20	83	6.7	758 1 VEGC_HUMAN	P01854 homo sapien
21	82	6.6	2167 1 SHK1_RAT	O9wv48 rattus norv
22	81.5	6.6	488 1 MM11_HUMAN	P24247 homo sapien
23	81.5	6.6	591 1 MNT_MOUSE	O08789 mus musculu
24	81.5	6.6	2124 1 Y192_HUMAN	O93074 homo sapien
25	81	6.5	283 1 ARF5_MOUSE	O70191 mus musculu
26	81	6.5	387 1 SGCA_MOUSE	P82350 mus musculu
27	81	6.5	428 1 EPC_HUMAN	P01854 homo sapien
28	81	6.5	1248 1 DIAL_HUMAN	O60610 homo sapien
29	80.5	6.5	1402 1 IF4G_RABIT	P41110 oryctolagus
30	80	6.4	397 1 CERD_STRCL	P18459 streptomyce
31	80	6.4	940 1 GBR2_RAT	O88871 rattus norv
32	80	6.4	1174 1 KPC1_COCHIE	O42632 cochliobolu
33	80	6.4	1794 1 YAVI1_SCHPO	O10172 schizosacch

34	79	6.4	805 1 YGM6_YEAST	P53086 saccharomyce
35	78.5	6.3	251 1 HXB4_HUMAN	P17483 homo sapien
36	78.5	6.3	382 1 AYVB_RAT	P38445 rattus norv
37	78.5	6.3	387 1 SGCA_RABIT	O28686 oryctolagus
38	78.5	6.3	913 1 DDRI1_HUMAN	O08345 h epithelia
39	78.5	6.3	1180 1 ATYL_HUMAN	O9nq11 homo sapien
40	78	6.3	205 1 CYSR_SYNY3	O55854 synchocyst
41	78	6.3	566 1 TS13_MOUSE	O01755 mus musculu
42	77.5	6.2	341 1 PLSX_VIBCH	O9kq44 vibrio chol
43	77.5	6.2	1885 1 FAS2_CANAL	P43098 c fatty aci
44	77.5	6.2	2004 1 M02_HUMAN	O92794 homo sapien
45	77	6.2	195 1 CORA_HPBVE	P29178 hepatitis b

ALIGNMENTS

RESULT 1	#	STANDARD	PRT	235 AA
FLJ3L_HUMAN				
ID	FLJ3L_HUMAN			
AC	P49771			
DT	01-OCT-1996 (rel. 34, Created)			
DT	01-OCT-1996 (rel. 34, Last sequence update)			
DT	15-JUN-2002 (rel. 41, Last annotation update)			
DE	SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3 ligand) (Flt3l).			
GN	FLT3LG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	(1)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94195428; PubMed=8145851;			
RA	Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,			
RA	Bazan J.F., Kastelein R., Hudak S., Wagner J., Watson J., Luh J.,			
RA	Duda G., Martini N., Peterson D., Menon S., Shanafelt A.,			
RA	Muench M., Kellner G., Nankikawa R., Renick D., Roncero M.G.,			
RA	Zlotnik A., Rosen O., Dubreuil P., Birnbaum D., Lee F.,			
RT	Ligand for FLT3/FLT3 receptor tyrosine kinase regulates growth of			
RT	haematopoietic stem cells and is encoded by variant RNAs.;			
RL	Nature 368:643-648(1994).			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94235842; PubMed=8180375;			
RA	Lyman S.D., James L., Johnson L., Brasel K., de Vries P.,			
RA	Escobar S., Downey H., Spielt R.R., Beckmann M.P., McKenna H.J.;			
RT	Cloning of the human homologue of the murine flt3 ligand: a growth			
RT	factor for early hematopoietic progenitor cells.;			
RL	Blood 83:2795-2801(1994).			
RN	(3)			
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.			
RX	MEDLINE=96032581; PubMed=7566977;			
RA	Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,			
RA	Escobar S.;			
RT	"Structural analysis of human and murine flt3 ligand genomic loci.;"			
RL	Oncogene 11:1165-1172(1995).			
RN	(4)			
RP	X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).			
RX	MEDLINE=20343011; PubMed=10881197;			
RA	Savvides S.N., Boone T., Karpus P.A.;			
RT	"Flt3 ligand structure and unexpected commonalities of helical			
RT	bundles and cystine knots.;"			
RL	Nat. Struct. Biol. 7:486-491(2000).			
CC	-1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC			
CC	CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING			
CC	FACTORS AND INTERLEUKINS.			
CC	-1- SUBUNIT: Homodimer (isoform 2).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);			
CC	secreted (isoform 2).			
CC	-1- ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here)			
CC	and 2/soluble; are produced by alternative splicing.			

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DR EMBL: U04806; AAA17999.1; -
 DR EMBL: U03858; AAA18825.1; -
 DR EMBL: U29874; AAA90949.1; -
 DR EMBL: U29874; AAA90950.1; -
 DR PDB: 1ETE; 09-JUN-00.
 DR Genew: HGNC:3766; FLT3LG.
 DR MIM: 600007; -
 DR InterPro: IPR004213; FLT3_1lg.
 DR Pfam: PF02947; flt3_1lg; 1.
 KM Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal;
 KM 3D-structure: 1

FT SIGNAL 26 POTENTIAL.
 FT CHAIN 27 235 SL CYTOKINE.
 FT DOMAIN 27 184 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 185 205 POTENTIAL.
 FT DOMAIN 206 235 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 30 111
 FT DISULFID 70 153
 FT DISULFID 119 158
 FT CARBOHYD 126 126
 FT CARBOHYD 149 149
 FT VARSPPLIC 161 178
 FT FT
 FT VARSPPLIC 179 235
 FT CONFLICT 72 72
 FT SEQUNCE 235 AA; 26416 MW; 73895BF693B4C6CF CRC64;

Query Match 100.0%; Score 1242; DR 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1,1e-96;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTAPAMPSTTYLLLLLSGLSGTQDSFQHSPISSDFAVKIRELSYLLQDYVTV 60
 Db 1 MVTAPAMPSTTYLLLLLSGLSGTQDSFQHSPISSDFAVKIRELSYLLQDYVTV 60

QY 61 ASNLODEELCGGMRVLAQRMERLKVAGSKMGLLEVTNEIHFVTKCAQPPESC. 120
 Db 61 ASNLODEELCGGMRVLAQRMERLKVAGSKMGLLEVTNEIHFVTKCAQPPESC. 120

QY 121 RFVQTNISRLLOETSEQLVAKPMTTRONFSRCLLEOCOPDSSSTLPPMSRPLEATPT 180
 Db 121 RFVQTNISRLLOETSEQLVAKPMTTRONFSRCLLEOCOPDSSSTLPPMSRPLEATPT 180

QY 181 APQPLLILLLLVGLLLAAAWCLHMORTRRTPRPGEOVPVPSQDILLVEH 235
 Db 181 APQPLLILLLLVGLLLAAAWCLHMORTRRTPRPGEOVPVPSQDILLVEH 235

RESULT 2
 FL3L_MOUSE
 ID FL3L_MOUSE STANDARD; PRT; 232 AA.
 AC P49772; 064085;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (FLT3
 DE ligand) (Flt3l).
 GN FL3LG OR FLT3L.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID:10090;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE:94195428; PubMed:8145851;

RA Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
 RA Bazar J.F., Kastlein R., Hudak S., Wagner J., Mattson J., Luh J.,
 RA Duda G., Martina N., Peterson D., Menon S., Shanfield A.,
 RA Muench M., Keiner G., Nankawa R., Kennick D., Roncarolo M.G.,
 RA Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.,
 RA "Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
 RA hematopoietic stem cells and is encoded by variant RNAs.";
 RA Nature 368:643-648(1994).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN-SUL/J;
 RC MEDLINE:94084791; PubMed:7505204;
 RX Lyman S.D., James L., Vandenbos T., Devries P., Brasel K.,
 RA Gliniak B., Hollingsworth L.T., Picha K.S., McKenna H.J.,
 RA Spielt R.R., Fletcher F.A., Maraskovsky E., Farrah T.,
 RA Foxworth D., Williams D.E., Beckmann M.P.,
 RA "Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase
 RA receptor: a proliferative factor for primitive hematopoietic cells.";
 RA Cell 75:1157-1167(1993).
 RL [3]
 RN SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RP MEDLINE:96032581; PubMed:7566977;
 RX Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
 RA Escobar S.;
 RA "Structural analysis of human and murine flt3 ligand genomic loci.";
 RA Oncogene 11:1165-1172(1995).
 RL [4]
 RN SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
 RP MEDLINE:95124710; PubMed:7824267;
 RX Lyman S.D., James L., Downey H., de Vries P.,
 RA Brasel K., Stocking K., Beckmann M.P., Copeland N.G.,
 RA Cleveland L.S.;
 RA "Identification of soluble and membrane-bound isoforms of the murine
 RA flt3 ligand generated by alternative splicing of mRNAs.";
 RA Oncogene 10:149-157(1995).
 RL [5]
 RN SEQUENCE FROM N.A.
 RP McClanahan T., Culpepper J., Campbell D., Wagner J.,
 RA Franz-Bacon K., Mattson J., Tsai S., Luh J., Guimares M.J.,
 RA Mettel M.-G., Rosnet O., Birnbaum D., Hannum C.;
 RA Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
 CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
 CC FACTORS AND INTERLEUKINS.
 CC -1- SUBUNIT: Homodimer (soluble isoform) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Two soluble
 CC isoforms are also produced by alternative splicing. One of which,
 CC 4/Edelta16, is biologically active, while the other, isoform
 CC 4/Edelta16, is inactive.
 CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; 1/6C (shown here), 2/5H, 3/E6
 CC and 4/Edelta16; are produced by alternative splicing
 CC -----
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DR EMBL: U04807; AAA18000.1; -
 DR EMBL: L23636; AAA39436.1; -
 DR EMBL: U29875; AAA90951.1; -
 DR EMBL: U29875; AAA90952.1; -
 DR EMBL: S76459; AAB33068.1; -
 DR EMBL: S76461; AAB33070.1; -
 DR EMBL: S76464; AAB33071.1; -
 DR EMBL: U44024; AAA93307.1; -
 DR EMBL: U44024; AAA93306.1; -
 DR MGD: MGI:95560; Flt3l.
 DR InterPro: IPR004213; Flt3_1lg.
 DR Pfam: PF02947; flt3_1lg; 1.
 KM Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal.

DR EMBL: X04370; CAA27895.1; -
DR PIR: C27342; TNBE12.
DR InterPro: IPR005051; Herpes_UL46.
DR Pfam: PF03387; Herpes_UL46_1.
DR Transcription regulation; Trans-acting factor.
SO SEQUENCE 661 AA; 74272 MW; GSCAV77AL6D365379 CRC64;

Query Match 7.4%; Score 92; DB 1; Length 661;
Best Local Similarity 26.6%; Pred. NO. 2.7;
Matches 61; Conservative 29; Mismatches 103; Indels 36; Gaps 11;

QY 19 LLSGLSTODCS---FQHSPISSDFAVKI--RELSDYLLDDYPTVAASNLQDELQCG-71
Db LTPSPVAGSTERSHYVLLGLHHNNVPESLVYSCMSNDVHDQFMQRYMETIQRCLDLDKLSGD 138
79
QY 72 GLMRLVLAQRMRERKATYAGSGMOLLERVN-----TEHHPTKCAFPD---PPSCLEFV 123
Db GLM+VYVENTWQYIKYTTGAEVPVTSKVNKKSKSTVLLSSVVAANPISRHPRKSKVI 197
139
QY 124 QTNISRLQETSEQVAVLKPRITRQNFRCLELQCGPPSTPRPWPSP-RPLEATAPAP 182
Db NSDYGICQELREALGAVQKIV--YFNR-----PDDPTNPSPDTRIRVOEIAAYTAT 247
198
QY 183 QPFLLLLLLPVGLLLLAAMCLHMQRTRRTPREGEQVPPVPSPDQL 231
Db GYGMWLMFLDYVD-----ARVCRHLKLFERRIRGRASV---IPDDLL 287
248

RESULT 4
GBR2_HUMAN
ID GBR2_HUMAN STANDARD; PRT; 941 AA.
AC 075899; 075974; 075975; 09UN9; 09UNR1; 09P1R2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Gamma-aminobutylic acid type B receptor, subunit 2 precursor (GABA-B
DE receptor 2) (GABA-B-R2) (Gb2) (GABABR2) (G protein-coupled receptor
DE 51) (GPR 51) (HG20).
GN GABBR2 OR GPR51.
GN OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Cerebellum;
RX MEDLINE=99087321; PubMed=9872216;
RA White J.H., Wise A., Main M.J., Green A., Fraser N.J., Disney G.H.,
RA Barnes A.A., Emson P., Foord S.M., Marshall F.H.;
RT "Heterodimerization is required for the formation of a functional
RT GABA(B) receptor";
RL Nature 356:679-682(1998).
RN [2]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 2A; 2B AND 2C).
RC TISSUE=Brain;
RX MEDLINE=20193514; PubMed=10727622;
RA Clark J.A., Mezey E., Lam A.S., Bonner T.I.;
RL "Distribution of the GABA(B) receptor subunit gb2 in rat CNS";
RN Brain Res. 860:41-52(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RA Liu M., Parker R., McCrea K., Watson J., Baker E., Sutherland G.,
RA Herzog H.;
RT "Cloning and characterization of a novel human GABA-B receptor subtype
RT with high affinity for GABA and low affinity for baclofen";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2A).
RC TISSUE=Hippocampus;
RA Borowsky B., Laz T., Gerald C.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2A).

CC TISSUE-Fetal brain; PubMed-10087195;
 CC MEDLINE-99189236; PubMed-10087195;
 CC Ng G.Y.K., McDonald T., Bonnett T., Rigby M., Heavens R., Whiting P.,
 CC Chateauf A., Coulombe N., Kargman S., Caskey T., Evans J.F.,
 CC O'Neill G.P., Liu Q.;
 CC "Cloning of a novel G-protein-coupled receptor GPR 51 resembling GABAB
 CC receptors expressed predominantly in nervous tissues and mapped
 CC proximal to the hereditary sensory neuropathy type 1 locus on
 CC chromosome 9.";
 CC Genomics 56:288-295(1999).
 CC [6]
 CC SEQUENCE FROM N.A. (ISOFORM 2A), AND VARIANTS PHE-628 AND ALA-869.
 CC TISSUE-Brain;
 CC MEDLINE-99263199; PubMed-10328880;
 CC Martin S.C., Russek S.J., Farb D.H.,
 CC "Molecular identification of the human GABABR2: cell surface
 CC expression and coupling to adenylyl cyclase in the absence of
 CC GABABR1.";
 CC Mol. Cell. Neurosci. 13:180-191(1999).
 CC [7]
 CC R1A-R2 INTERACTION.
 CC MEDLINE-99175124; PubMed-10075644;
 CC Ng G.Y.K., Clark J., Coulombe N., Ethier N., Hebert T.E., Sullivan R.,
 CC Kargman S., Chateauf A., Tsukamoto N., McDonald T., Whiting P.,
 CC Mezey E., Johnson M.P., Liu Q., Kolakowski L.F. Jr., Evans J.F.,
 CC Bonner T.I., O'Neill G.P.;
 CC "Identification of a GABAB receptor subunit, gb2, required for
 CC functional GABAB receptor activity.";
 CC J. Biol. Chem. 274:7607-7610(1999).
 CC [8]
 CC R1A-R2 INTERACTION.
 CC MEDLINE-20237752; PubMed-10773016;
 CC Sullivan R., Chateauf A., Coulombe N., Kolakowski L.F. Jr.,
 CC Johnson M.P., Hebert T.E., Ethier N., Belley M., Metters K.,
 CC Abramowitz M., O'Neill G.P., Ng G.Y.K.;
 CC "Coexpression of full-length gamma-aminobutyric Acid(B) (GABA(B))
 CC receptors with truncated receptors and metabotropic glutamate
 CC receptor 4 supports the GABA(B) heterodimer as the functional
 CC receptor.";
 CC J. Pharmacol. Exp. Ther. 293:460-467(2000).
 CC -1- FUNCTION: RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM CHANNELS AND MODULATES
 CC INSITUT PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE
 CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS. WHEREAS POSTSYNAPTIC
 CC GABA-B-R DECREASE NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND
 CC ANTI-NOCEPTION.
 CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO
 CC HAPPEN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A
 CC PREREQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE
 CC PLASMA MEMBRANE.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2A (SHOWN HERE), 2B AND 2C; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN
 CC CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND
 CC TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS
 CC CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD AMYGDALA AND MEDULLA.
 CC WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.
 CC -1- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
 CC GABA-B RECEPTOR SUBFAMILY.
 CC -----

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 CC -----
 CC DR EMBL: A0102188; CAA09942.1; -
 CC DR EMBL: AF056085; AAC63228.1; -
 CC DR EMBL: AF095723; AAC63383.1; -
 CC DR EMBL: AF095724; AAC63384.1; -
 CC DR EMBL: AF095784; AAD30389.1; -
 CC DR EMBL: AF074483; AAD03336.1; -
 CC DR EMBL: AF069755; AAC99345.1; -
 CC DR EMBL: AF099033; AAD45867.1; -
 CC DR Genew: HGNC:4507; GPR51.
 CC DR InterPro: IPR001828; ANF_receptor.
 CC DR InterPro: IPR000337; GPCR_Mgr.
 CC DR Pfam: PF01094; ANF_receptor; 1.
 CC DR PROSITE: PS00979; G-PROTEIN_RECEP_F3_1; FALSE_NEG.
 CC DR PROSITE: PS00980; G-PROTEIN_RECEP_F3_2; FALSE_NEG.
 CC DR PROSITE: PS00981; G-PROTEIN_RECEP_F3_3; FALSE_NEG.
 CC DR PROSITE: PS50259; G-PROTEIN_RECEP_F3_4; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
 CC Postsynaptic membrane; Collid coil; Alternative splicing;
 CC Polymorphism.
 CC FT SIGNAL 1 41
 CC FT CHAIN 42 941
 CC FT
 CC FT DOMAIN 42 483
 CC FT TRANSMEM 484 504
 CC FT DOMAIN 505 522
 CC FT TRANSMEM 523 543
 CC FT DOMAIN 544 551
 CC FT TRANSMEM 552 572
 CC FT DOMAIN 573 597
 CC FT TRANSMEM 598 618
 CC FT DOMAIN 619 654
 CC FT TRANSMEM 655 675
 CC FT DOMAIN 676 691
 CC FT TRANSMEM 692 712
 CC FT DOMAIN 713 720
 CC FT TRANSMEM 721 741
 CC FT DOMAIN 742 941
 CC FT DOMAIN 781 819
 CC FT CARBOHYD 90 90
 CC FT CARBOHYD 298 298
 CC FT CARBOHYD 389 389
 CC FT CARBOHYD 404 404
 CC FT CARBOHYD 453 453
 CC FT VARSPLIC 902 927
 CC FT VARSPLIC 929 941
 CC FT
 CC FT VARIANT 628 628
 CC FT
 CC FT VARIANT 869 869
 CC FT
 CC FT VARIANT 869 869
 CC FT
 CC FT CONFLICT 6 6
 CC FT CONFLICT 12 12
 CC FT CONFLICT 424 424
 CC FT
 CC SO SEQUENCE 941 AA; 105821 MW; 09P1773DB0673C5D CRC64;
 CC
 CC Query Match 7.2%; Score 89.5; DB 1; Length 941;
 CC Best Local Similarity 44.1%; Pred. No. 6.4;
 CC Matches 26; Conservative 2; Mismatches 22; Indels 9; Gaps 3;
 CC
 CC OY 170 SPRLPEATAPTAOPP-----LILLILLPVGLLLAAMCMLHMRTRRRPRGEQVPPV 224
 CC DB 3 SRRSQGPGRPPPPPPPPPPARLLILLPLPLPLAPGAM--GM--ARKGAPRPPSSPL 56

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RESULT 5
SCCA_MESAU
ID SCCA_MESAU STANDARD: PRT: 387 AA.
AC 064255:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Alpha-sarcoglycan precursor (Alpha-SG) (Adhalin) (50 kDa dystrophin-
associated glycoprotein) (50DAG).
GN SGCA.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
ON NCBI_Taxid=10036;
RX 11)
RP SEQUENCE FROM N.A.
RC STRAIN=Syrian; TISSUE=Heart muscle;
RX MEDLINE=98054328; PubMed=9391120;
RA Sakamoto A., Ono K., Abe M., Jasmijn G., Eki T., Murakami Y.,
RA Masaki T., Toyooka T., Hanaoka F.;
RT "Both hypertrophic and dilated cardiomyopathies are caused by mutation
RT of the same gene, delta-sarcoglycan, in hamster: an animal model of
RT disrupted dystrophin-associated glycoprotein complex."
RL Proc. Natl. Acad. Sci. U.S.A. 94:13873-13878(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FiB; TISSUE=Skeletal muscle;
RX MEDLINE=95278335; PubMed=7758576;
RA Roberts S.L., Campbell K.P.;
RA "Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic
RT hamster."
RL FEBS Lett. 364:245-249(1995).
CC -1- FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A SUBCOMPLEX OF
CC THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A LINK BETWEEN THE
CC F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Sarcolemmal
CC (potential).
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKELETAL AND
CC HEART MUSCLE.
CC -1- SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY.
CC
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CC
DR EMBL: D83651; BAA12025.1;
DR EMBL: U21677; AAA81645.1;
KW Cytoskeleton; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 387 ALPHA-SARCOGLYCAN.
FT DOMAIN 24 290 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 291 311 POTENTIAL.
FT DOMAIN 312 387 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 209 335 CYS-RICH.
FT CARBOHYD 174 174 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAc. . .) (POTENTIAL).
SQ SEQUENCE 387 AA; 43326 MW; D8599C0FAF646C3F CRC64;

Query Match 7.28; Score 89; DB 1; Length 387;
Best Local Similarity 23.48; Pred. NO. 2.6;
Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

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DB 162 GGLMELGELQINTSALDRGRVPLPIGRKRGVYIKVGSATPFSTCLKWVAPDSYAR 221
QY 111 CAFOPPP--SC-----LRFVOTNISRLQETSEQVALKRWITQNSRCLQECOD 161
DB 222 CAGOGPPLLCYDSDLAPHRFVDMCNVSLVDKSVPELD-----EVPDPD 266
QY 162 SSTLPPEPMSRPLEAT-----APPAPOPPLLLLLLVGLLLLAAMC----- 204
DB 267 GLEHHPFPFCPPFEATGRGFDLADALVTLVPLVALL---TLLLVYIMCRREGQLKD 323
QY 205 -----LHMQTRRRTPRP-----GEOVPP-VPSPQ-DLL 231
DB 324 MATSDIQVHCHTGHNTFEELRQMARREYPRSLTPMENVATGGRPLPRVDSQAVPL 383
QY 232 LVKH 235
DB 384 LDQH 387

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RESULT 6
SC3AL_HUMAN
ID SC3AL_HUMAN STANDARD: PRT: 793 AA.
AC Q15459;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Splicing factor 3 subunit 1 (Spliceosome associated protein 114) (SAP
DE 114) (SP3a120).
GN SP3A1 OR SAP114.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ON NCBI_Taxid=9606;
RX [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96079958; PubMed=7489498;
RA Kraemer A., Mulhauser F., Wersig C., Groning K., Bilbe G.;
RT "Mammalian splicing factor SF3a120 represents a new member of the
RT SUPR family of proteins and is homologous to the essential splicing
RT factor PRP21P of Saccharomyces cerevisiae."
RL RNA 1:260-272(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Baare D.M.,
RA Clamp M., Smink L.J., Alnscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Graffam D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.P., Leversha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashneghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurtry A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Mioshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shitani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,
RA Roe B.A., Chen F., Chu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.T.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malay E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,

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RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Biedshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Letresse P., Layman D., Ozersky P., Rohlfing T.,
 RA Schert P., Walker C., Wamsley A., Woldmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L., Marais E., Waterston R., Wilson R.,
 RA Emanuel B.S., Shaikh T., Kurchashv H., Salita S., Budarf M.L.,
 RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
 RA Kim U.J., Shiyaya H., Simon M.I., Dumasht J.P., Peyrard M., Kedra D.,
 RA Seroussi E., Franssen I., Tapia I., Bruder C.E., O'Brien K.P.,
 RA Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
 RA Tilahun Y., Wright H.,
 RA The DNA sequence of human chromosome 22." ;
 RA Nature 402:489-495(1999).
 [3]
 RP CHARACTERIZATION OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'
 RP MEDLINE:20337962; PubMed:10882114;
 RA Das R., Zhou Z., Reed R.;
 RT Functional association of U2 snRNP with the ATP-independent
 RT spliceosomal complex E." ;
 RT Mol. Cell 5:779-787(2000).
 CC -1- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SF3A REQUIRED FOR 'A'
 CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE
 CC BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT
 CC BINDING OF SF3A/SF3B COMPLEX UPSTREAM OF THE BRANCH SITE IS
 CC ESSENTIAL. IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE
 CC INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.
 CC -1- SUBUNIT: COMPONENT OF SPLICING FACTOR SF3A WHICH IS COMPOSED OF
 CC THREE SUBUNITS: SF3A3/SAP61, SF3A2/SAP62, SF3A1/SAP14. SF3A
 CC ASSOCIATES WITH THE SPLICING FACTOR SF3B AND A 12S RNA UNIT TO
 CC FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP).
 CC INTERACTS WITH SF3A3.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
 CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.
 CC -1- SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.
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 CC -----
 DR EMBL: X85237; CAA59494.1; -
 DR EMBL: AC004997; AAC23435.1; -
 DR HSSP: 015843; 1ND0.
 DR GeneW: HGNC:10765; SF3A1.
 DR MIM: 605395; -
 DR InterPro: IPR000061; Surp.
 DR InterPro: IPR000626; Ubiquitin.
 DR Pfam: PF00240; ubiquitin.1.
 DR Pfam: PF01805; Surp. 2.
 DR SMART: SM00213; UBQ.1.
 DR PROSITE: PS50053; UBIQUITIN_2.1.
 DR KMW: SUBCELLULAR LOCATION: Type I membrane protein; Repeat.
 FT REPEAT 52 94
 FT REPEAT 166 793
 FT DOMAIN 707 793 UBIQUITIN-LIKE.
 FT DOMAIN 10 16 POLY-PRO.
 FT DOMAIN 118 122 POLY-GLN.
 FT DOMAIN 260 267 POLY-GLU.
 FT DOMAIN 369 372 POLY-PRO.
 FT DOMAIN 557 560 POLY-PRO.
 FT DOMAIN 672 675 POLY-PRO.
 SO SEQUENCE 793 AA: 88886 MM: 7259PBC4577305C CRC64;
 Query Match 7.2%; Score 89; DB 1; Length 793;
 Best Local Similarity 22.3%; Pred. No. 5.8;
 Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

DB 401 LPPAPAPDEXLV-----SPITGE--KI-----PASK 424
 QY 64 LQDEELCGGIMRYLVLAQRME-RLKTV-----AGSKQGLLENNTEIHF 107
 DB 425 MOCHMRIG-----LLPRVMEQDRDSIREKQSDDEVYAPGLDISSLSKQLAER-RTDIFG 478
 QY 108 VTRCA-----POPPSCLEFR-----VOTNISRLQETSGLVALPWI 145
 DB 479 VETAIQKRTIGEREIQKPEKRVWDGSGSMARQQAQANIT--LQDQLEAIHKAGLV 536
 QY 146 ---TRQNF---SRCLELQCP-----DSSLTLP-----PWSDRPLEAT---APT 180
 DB 537 PEDDTKEKIGSKPNEIPQPPSSATNIPSSAPITSVPRPTMPDPVRTVAVAPV 596
 QY 181 APPPLLLLLLVGLLLAANCLHQRR-----RRPRGEOVPP---VSP 227
 DB 597 MPRPPAVSVVRLPPGSVIAPMPPIIHAPRINVVMPSPAPPIAPRPPMIVPAFVAP 656
 RESULT 7
 TNR3_MOUSE
 ID TNR3_MOUSE STANDARD: PRT; 415 AA.
 AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (Lymphotoxin-beta receptor).
 GN LTBR OR TNFRSF3 OR TNFCR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CVB; TISSUE=Lung;
 RX MEDLINE:96072804; PubMed:7594541;
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.;
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 RT and expression." ;
 RT J. Immunol. 155:5280-5288(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:96163885; PubMed-8586432;
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 RA Honjo T.;
 RT "The murine lymphotoxin-beta receptor cDNA: Isolation by the signal
 RT sequence trap and chromosomal mapping." ;
 RT Genomics 30:312-319(1995).
 CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTA and LTB, and for TNFSF4/LIGHT. Promotes apoptosis via TRAF3
 CC and TRAF5. May play a role in the development of lymphoid organs
 CC (By similarity).
 CC -1- SUBUNIT: Self-associates (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
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 CC -----
 DR EMBL: U29173; AAA68964.1; -
 DR EMBL: L38423; AAB00846.1; -
 DR EMBL: U30798; AAB1334.1; -
 DR HSSP: 014763; 1D0G.
 DR MGD: MGI:104875; Ltbr.
 DR InterPro: IPR001368; TNFR_c6.

RT identifies two cell cycle genes from *Drosophila*: a cdc2 homologue and
RT string".
RL EMBO J. 9:3565-3571(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Berkeley;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriel J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan J.P., Bhargava P., Boldt R.,
RA Borkov A., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burks K.C., Busam D.A., Butler H., Cadenot E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
RA Jajalal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
RA Laspo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: THIS PROTEIN FUNCTIONS AS A DOSAGE-DEPENDENT INDUCER IN
CC MITOTIC CONTROL. IT IS A TYROSINE PROTEIN PHOSPHATASE RECRUITED FOR
CC PROGRESSION OF THE CELL CYCLE. IT MAY DIRECTLY DEPHOSPHORYLATE
CC P34(CDC2) AND ACTIVATE THE P34(CDC2) KINASE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: protein tyrosine phosphatase + H(2)O -> protein
CC tyrosine + phosphate.
CC -1- SIMILARITY: BELONGS TO THE MPI PHOSPHATASE FAMILY.
CC -1- SIMILARITY: CONTAINS 1 RHODANESE DOMAIN.
CC -----
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CC or send an email to license@1sb-sib.ch).
CC -----
DR EMBL, M24909, AAA28916.1, -
DR EMBL, X57495, CAA40732.1, -
DR EMBL, AE003768, AAF56885.1, -
DR PIR, A32290, A32290.
DR PIR, S12008, S12008.
DR HSP, P30304, I025.
DR PDBase, FBgn0003525, stg
DR InterPro, IPR000751, MPI_Phosphatase
DR InterPro, IPR001753, Rhodanese-like.
DR Pfam, PF00581, Rhodanese; 1.
DR PRINTS, PR00716, MPIPHPTASE.

DR SMART; SM00450; RHOD. 1.
 KW Cell division; Mitosis; Hydrolase.
 FT DOMAIN 319 430 RHODANSE.
 FT ACT_SITE 379 379 BY SIMILARITY.
 FT CONFLICT 228 228 A -> T (IN REF. 1)
 SQ SEQUENCE 479 AA; 54094 MW; 68483f3a285962cc CRC64;

Query Match 7.0%; Score 87.5; DB 1; Length 479;
 Best Local Similarity 22.9%; Pred. No. 4.4;
 Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;

QY 1 MYVLAPAMPTTYLL---LLLSGLSTOCSTQHSISSDPVAKINELSDYLQDYP 57
 DB 72 MLLSPGSPQFQIVROPKILPAMGVSS-----DHTRPARS-FRI-FNLSLS-----T 117
 QY 58 VIVASNLQDEELGGLMLRVLQRMWRERLKVAGSKMGLLRVNTVEHFVRCARQPP 117
 DB 118 CMESMSMDE-----TMELFEMSOSO-----QTALCF-----P 146
 QY 118 SCLRFVQVNIISLQETSEQLVALRP---WTRONFSRCLEL-QCOPDSSTLPPMSPRP 173
 DB 147 SCIN-----SLISQIIEQPAKSPAGLSMRSPVRCLSMTESNTNTTTPPKTPE- 199
 QY 174 LEATAPTA---POPULLLLLPVGLLLLAAMCLHMQTRRRTPRGQVPPVSPDL 230
 DB 200 ---TARDCKRPEP-----ASANGSPISQKRHRCAVENCNPAPPSLQ 242
 QY 231 LLYEH 235
 DB 243 VTISH 247

RESULT 9
 DDRL_RAT STANDARD: PRT; 910 AA.
 AC 063474;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112)
 DE (Tyrosine-protein kinase CCK) (Cell adhesion kinase) (Tyrosine kinase
 DE DDR) (Discoidin receptor tyrosine kinase) (Protein-tyrosine kinase
 DE PTK-3).
 GN DDRL OR EDDRL OR PTK3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Brain;
 RX MEDLINE=94179320; PubMed=8127887;
 RA Sanchez M.P., Tapley P., Saint S.S., He B., Pulido D., Barbacid M.;
 RT "Multiple tyrosine protein kinases in rat hippocampal neurons: isolation of ptk-3, a receptor expressed in proliferative zones of the developing brain.";
 RT Proc. Natl. Acad. Sci. U.S.A. 91:1819-1823(1994).
 RL -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND RECOGNITION (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: VARIOUS EMBRYONIC AND ADULT TISSUES; ALSO PROLIFERATIVE ZONES OF THE DEVELOPING BRAIN; HIPPOCAMPAL NEURONS.
 CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN RECEPTOR SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; I26525; AAA21089.1; -
 DR HSSP; P00523; 2PTK.
 DR InterPro: IPR000719; Euk.pkinase.
 DR InterPro: IPR000421; FAS8_C.
 DR InterPro: IPR002011; RTKkinaseII.
 DR InterPro: IPR001245; Tyr.pkinase.
 DR Pfam; PF00754; F5_F8_type_C; 1.
 DR ProDom; PD000001; Euk.pkinase; 1.
 DR SMART; SM00231; FA58C; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR PROSITE; PS01285; FA58C_1; 1.
 DR PROSITE; PS01286; FA58C_2; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Phosphorylation; Tyrosine-protein kinase; Glycoprotein; Signal;
 FT PHOSPHORYLATION; Transmembrane; Receptor; ATP-binding.
 FT SIGNAL 1 19
 FT CHAIN 20 910
 FT DOMAIN 20 413
 FT TRANSMEM 414 440
 FT DOMAIN 441 910
 FT DOMAIN 32 186
 FT DOMAIN 378 412
 FT DOMAIN 473 598
 FT DOMAIN 607 902
 FT NP_BIND 613 621
 FT BINDING 652 652
 FT ACT_SITE 763 763
 FT DISULFID 32 166
 FT MOD_RES 510 510
 FT MOD_RES 789 789
 FT MOD_RES 793 793
 FT MOD_RES 794 794
 FT CARBOHYD 212 212
 FT CARBOHYD 261 261
 FT CARBOHYD 371 371
 FT CARBOHYD 391 391
 SQ SEQUENCE 910 AA; 101164 MW; 7E7FFA1DCB029806 CRC64;

Query Match 7.0%; Score 87; DB 1; Length 910;
 Best Local Similarity 24.5%; Pred. No. 10;
 Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;

QY 143 PVTTRNFNSRCLELQCPDSTLTP-PW---SPRPLEATA-----PTRAP----- 184
 DB 356 PWLSEISFISDV-VNDSDTFPPAPWPPGPPPTNFSSLELEPRGQPVANAEGSPTA 414
 QY 185 -----PLLLLLLPVGLLLLAAMCLHMOR-----TRRR-----T 214
 DB 415 ILICGLVAILLLLLIALLML-----WRLHRRLLSKAERVLEELVHLSVPGDITLIN 470
 QY 215 PRPGGVPP-----VSPDILL 232
 DB 471 NRPGRPEPPVQEPFRGTPTHSAPCVNGSALLL 505

RESULT 10
 DDRL_MOUSE STANDARD: PRT; 911 AA.
 AC 003146;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112)
 DE (Tyrosine-protein kinase CCK) (Cell adhesion kinase) (Tyrosine kinase

DE (DDR) (Discoidin receptor tyrosine kinase) (Protein-tyrosine kinase
DE MKR-6).
GN DDR1 OR EDDR1 OR CAK OR MPK6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX STRAIN=C57BL/6;
RC MEDLINE=96204002; PubMed=8622863;
RA Perez J.L., Jing S.Q., Wong T.W.;
RT "Identification of two isoforms of the Cak receptor kinase that are
coexpressed in breast tumor cell lines."
RL Oncogene 12:1469-1477(1996).
RN [2]
RP SEQUENCE OF 766-822 FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Embryonic brain;
RC MEDLINE=93096484; PubMed=1281307;
RA Gliardi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.-G.,
RA Chester A., Wilkinson D.G., Charney P.;
RT "An Eph-related receptor protein tyrosine kinase gene segmentally
expressed in the developing mouse hindbrain."
RL Oncogene 7:2499-2506(1992).
CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
RECOGNITION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK I (SHOWN HERE) AND CAK II;
ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE
ABSENCE OF A 37 RESIDUES SEGMENT.
CC -1- TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK I, IS EXPRESSED IN
DEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXPRESSED IN VARIOUS
EPITHELIAL CELLS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. INSULIN
RECEPTOR SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 FS/8 TYPE C DOMAIN.
CC -----
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CC -----
DR EMBL: L57509; AAB05209.1; -;
DR EMBL: X57240; CAA0516.1; -;
DR PIR: S30502; S30502.
DR HSSP: P00523; 2PTK.
DR MGD: MGI:99216; Ddrl.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR000421; FASE_C.
DR InterPro: IPR002011; RTKinaseII.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: PF00069; Pkinase.1.
DR Pfam: PF00754; F5_F8_TypeC.1.
DR ProDom: PD0000001; Euk_Pkinase.1.
DR SMART: SM00231; FASEC.1.
DR SMART: SM00219; TYRC.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR.1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II.1.
DR PROSITE: PS01285; FASEC.1; 1.
DR PROSITE: PS01286; FASEC.2; 1.
DR Transferase: Tyrosine-protein kinase; Glycoprotein; Signal;
KW Phosphorylation; Transmembrane; Receptor; ATP-binding;
KW Alternative splicing.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 911 EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1.
FT DOMAIN 20 414 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 415 441 POTENTIAL.
FT DOMAIN 442 911 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 186 FS/8 TYPE C (PHOSPHOLIPID-BINDING,
POTENTIAL).
FT DOMAIN 379 413 GLY/PRO-RICH.
FT DOMAIN 474 599 GLY/PRO-RICH.
FT NP_BIND 608 903 PROTEIN KINASE.
FT BINDING 614 622 ATP (BY SIMILARITY).
FT ACT_SITE 653 653 ATP (BY SIMILARITY).
FT ACT_SITE 764 764 BY SIMILARITY.
FT MOD_RES 32 186 BY SIMILARITY.
FT MOD_RES 511 511 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 790 790 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 794 794 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 795 795 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 503 539 MISSING (IN ISOFORM CAK II).
SQ SEQUENCE 911 AA; 101160 MW; DBB7FE03DD79510 CnC64;
Query Match 7.0%; Score 87; DB 1; Length 911;
Best Local Similarity 24.5%; Pred. No. 10;
Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;
OY 143 PITRONEFRCLELOCQPSSTLPP-PW---SPRIEATA---PPADP----- 184
DB 357 PWLSEIFISDY-VNDSSTFPAPWPPPPPTNPSLELEPGQOPVAKAGSPRA 415
OY 185 -----PLLLLLPVGLLLAAMCLHMOR---TRRR-----T 214
DB 416 ILICCVAILLLILLIALML---WRLWRLLSAERVLEELTVLHVSVDGITLLIN 471
OY 215 PRPGQVPP-----VPSPODLL 232
DB 472 NRPGRPPPPYQEPNRPGRTPPHSAPCPVNGSALL 506
RESULT 11
CNC4_BOVIN STANDARD; PRT; 1394 AA.
ID CNC4_BOVIN Q28181; Q28082; Q03861;
AC Q28181; Q28082; Q03861;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 240 kDa protein of rod photoreceptor CNG-channel [contains: Glutamic
acid-rich protein (GARP); Cyclic-nucleotide-gated cation channel 4
(CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel
modulatory subunit)].
DE modulatory subunit)].
DE modulatory subunit)].
GN CNGB1 OR CNC4.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96009859; PubMed=7546742;
RA Goetz S., Colville C., Mueller F., Dose A., Godde M., Molday L.,
RA Kaupp U.B., Molday R.S.;
RT "A 240 kDa protein represents the complete beta subunit of the cyclic
nucleotide-gated channel from rod photoreceptor."
RL Neuron 15:627-636(1995).
RN [2]
RP SEQUENCE OF 454-1394 FROM N.A.
RC TISSUE-Testis;
RX MEDLINE=96198098; PubMed=8626431;
RA Biel M., Zong X., Ludwig A., Sauter A., Hofmann F.;
RT "Molecular cloning and expression of the modulatory subunit of the
J. Biol. Chem. 271:6349-6355(1996)."

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE CYCLIC-AMP-dependent transcription factor ATF-5 (Activating
 DE transcription factor 5) (Transcription factor ATF5).
 GN ATF5 OR ATF5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homalidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20558615; PubMed-11087824;
 RA White J.H., McIlhinney R.A.J., Wise A., Ciruela F., Chan W.Y.,
 RA Emson P.C., Billington A., Marshall F.H.;
 RT "The GABAB receptor interacts directly with the related transcription
 RT factors CREB2 and ATF5";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:13967-13972(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kohroki J., Tanaka K.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 161-282 FROM N.A.
 RX MEDLINE-99303793; PubMed-10373550;
 RA Patl D., Meistrich M.L., Pion S.E.;
 RT "Human Gc34 and Rad6b ubiquitin-conjugating enzymes target repressors
 RT of cyclic AMP-induced transcription for proteolysis";
 RL Mol. Cell. Biol. 19:5001-5013(1999).
 CC -1- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE)
 CC (CONSENSUS: 5'(GTGAGT(A/C)(A/G)-3'), A SEQUENCE PRESENT IN MANY
 CC VIRAL AND CELLULAR PROMOTERS.
 CC -1- SUBUNIT: BINDS DNA AS A DIMER (POTENTIAL). INTERACTS WITH GABAB
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE BZIP FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF305687; AAG22558.1; -
 DR EMBL: AB021663; BAA78477.2; -
 DR EMBL: AF101388; AAD28370.1; -
 DR TRANSFAC: T04877; -
 DR Genem: HGNC:790; ATF5.
 DR MIM: 606398; -
 DR InterPro: IPR004827; TF_BZIP.
 DR Pfam: PF00170; BZIP.1.
 DR SMART: SM00338; BRU2.1.
 DR PROSITE: PS00036; BZIP_BASIC.1.
 KM Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KM Multigene family.
 FT DOMAIN 123 139 POLY-PRO.
 FT DOMAIN 186 194 POLY-PRO.
 FT DOMAIN 210 230 BASIC MOTIF.
 FT DOMAIN 236 250 LEUCINE-ZIPPER (PROBABLE).
 FT CONFLICT 161 163 LLA -> RHE (IN REF. 3).
 SO SEQUENCE 282 AA; 30674 MW; DDB2F907CA0215A0 CAC64;
 Query Match 6.88; Score 85; DB 1; Length 282;
 Best Local Similarity 29.98; Pred. NO. 3.9;
 Matches 38; Conservative 7; Mismatches 38; Indels 44; Gaps 6;
 OY 144 WIT-RONSPRCLECCQDSTLPPMSPRP--LEATA-----178
 DB 66 WMTKRVDFIALPLPPLPPTLPP--SPTRPDLFAMASLKLKELEOMEDFLDAPPLPP 124
 OY 179 ---PTAPQPLLLLLLPVGL-----LLAAMCLH--WQTRRRTRPRGQ 220

DB 125 PSEPPPLPPLPAPSLPLSPSFDLPPPPVLTFLDLALAYCNNAEQGEVGMPLPPQ 184
 OY 221 VPPVSP 227
 DB 185 QPPPPSP 191
 RESULT 14
 FCGRN_RAT
 ID FCGRN_RAT STANDARD; PRT; 366 AA.
 AC P13599;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE IGG receptor FCGRN large subunit p51 precursor (FCRN) (Neonatal FC
 DE receptor) (IGG FC fragment receptor transporter, alpha chain).
 GN FCGRN OR FCGRN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX STRAIN-Miscari;
 RX MEDLINE-89097257; PubMed-2911353;
 RA Stimster N.E., Mostov K.E.;
 RT "An Fc receptor structurally related to MHC class I antigens";
 RL Nature 337:184-187(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Epithelium;
 RX MEDLINE-90315866; PubMed-2534798;
 RA Stimster N.E., Mostov K.E.;
 RT Cloning and expression of the neonatal rat intestinal Fc receptor, a
 RT major histocompatibility complex class I antigen homolog";
 RL Cold Spring Harb. Symp. Quant. Biol. 54:571-580(1989).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE-95059482; PubMed-7969498;
 RA Burneister W.P., Huber A.H., Bjorkman P.J.;
 RT "Crystal structure of the complex of rat neonatal Fc receptor with
 RT Fc";
 RL Nature 372:379-383(1994).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE-98154319; PubMed-9493268;
 RA Vaughn D.E., Bjorkman P.J.;
 RT "Structural basis of pH-dependent antibody binding by the neonatal Fc
 RT receptor";
 RL Structure 6:63-73(1998).
 CC -1- FUNCTION: BINDS TO THE FC REGION OF MONOMERIC IMMUNOGLOBULINS
 CC GAMMA. MEDIATES THE SELECTIVE UPTAKE OF IGG FROM MILK AND HELPS
 CC NEONATE ANIMALS TO ACQUIRE PASSIVE IMMUNITY. IGG IN THE MILK IS
 CC BOUND AT THE APICAL SURFACE OF THE INTESTINAL EPITHELIUM. THE
 CC RESULTANT FCGRN-IGG COMPLEXES ARE TRANSCYTOSED ACROSS THE
 CC INTESTINAL EPITHELIUM AND IGG IS RELEASED FROM FCGRN INTO BLOOD OR
 CC TISSUE FLUIDS (BY SIMILARITY).
 CC -1- SUBUNIT: FCGRN COMPLEX CONSIST OF TWO SUBUNITS: P51, AND P14 WHICH
 CC IS EQUIVALENT TO BETA-2-MICROGLOBULIN. IT FORMS AN MCH CLASS I-
 CC LIKE HETERODIMER.
 CC -1- TISSUE SPECIFICITY: INTESTINAL EPITHELIUM.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -----
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 CC -----

Query Match	6.88;	Score 85;	DB 1;	Length 366;
Best Local Similarity	22.28;	Pred. No. 5.2;		
Match 51; Conservative	21;	Mismatches	66;	Indels 92; Gaps 11

	RESULT	15
ABFL_MOUSE	ID	ABFL_MOUSE
	STANDARD:	PRT; 3726 AA.
AC	061329;	
DT	16-OCT-2001 (Rel. 40. Created)	
DT	16-OCT-2001 (Rel. 40. Last sequence update)	
DT	16-OCT-2001 (Rel. 40. Last annotation update)	
DE	Alpha-fetoprotein enhancer binding protein (AT motif-binding factor), De	
DE	alpha-fetoprotein enhancer binding protein (AT motif-binding factor 1).	
GN	ATBFl.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxId=10090;	
OX	(1)	
PC	SEQUENCE FROM N.A.	
RC	SRINAI-BALB/MK X ICR; TISSUE=Brain;	
RX	MEDLINE=96194902; PubMed=8654949;	
RX	Ito A., Miura Y., Watanabe M., Sakai M., Inoue Y., Hashimoto T., Morinaga T., Nishi S., Tamaki T.,	
RA		

RT	"Cloning of the cDNA encoding the mouse ATF1 transcription factor.";
RL	Gene 168:227-231(1996).
CC	-1- FUNCTION: Transcriptional activator that binds to the AT-rich core
CC	sequence of the enhancer element of the AFP gene.
CC	-1- SUBCELLULAR LOCATION: Nuclear.
CC	-1- SIMILARITY: CONTAINS 4 HOMEBOX DOMAINS.
CC	-----
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CC	or send an email to license@isb-sib.ch). -----
DR	EMBL; D26046; BAA05046.1; ..
DR	HSSP; P20263; IOCP.
DR	TRANSFAC; T03881; ..
DR	MCD; MGI:99948; Atbf1.
DR	InterPro; IPR001356; Homeobox.
DR	InterPro; IPR000822; Znf.C2H2.
DR	InterPro; IPR003604; Znf.U1.
DR	Pfam; PF00046; homeobox_4.
DR	Pfam; PF00096; zf-C2H2; 20.
DR	ProDom; PD000010; Homeobox; 4.
DR	SMART; SM00389; Hox; 4.
DR	SMART; SM00355; ZnF_C2H2; 22.
DR	SMART; SM00451; ZnF_U1; 7.
DR	PROSITE; PS00027; HOMEBOX_1; 2.
DR	PROSITE; PS00071; HOMEBOX_2; 4.
DR	PROSITE; PS00028; ZINC_FINGER_C2H2_1; 15.
DR	PROSITE; PS01057; ZINC_FINGER_C2H2_2; 9.
KW	Transcription regulation; Activator; Zinc-finger; Metal-binding;
KW	DNA-binding; Homeobox; Nuclear protein; Repeat.
FT	ZN_FING 79 103 C2H2-TYPE.
FT	ZN_FING 282 303 C2H2-TYPE.
FT	ZN_FING 641 664 C2H2-TYPE.
FT	ZN_FING 672 695 C2H2-TYPE.
FT	ZN_FING 727 751 C2H2-TYPE.
FT	ZN_FING 805 829 C2H2-TYPE (ATYPICAL).
FT	ZN_FING 946 969 C2H2-TYPE (DEGENERATE).
FT	ZN_FING 985 1009 C2H2-TYPE (ATYPICAL).
FT	ZN_FING 1041 1065 C2H2-TYPE (ATYPICAL).
FT	ZN_FING 1089 1113 C2H2-TYPE (ATYPICAL).
FT	ZN_FING 1233 1256 C2H2-TYPE (ATYPICAL).
FT	ZN_FING 1262 1295 C2H2-TYPE.
FT	ZN_FING 1370 1395 C2H2-TYPE.
FT	ZN_FING 1411 1433 C2H2-TYPE.
FT	ZN_FING 1439 1462 C2H2-TYPE.
FT	ZN_FING 1553 1579 C2H2-TYPE.
FT	ZN_FING 1606 1630 C2H2-TYPE.
FT	ZN_FING 1990 2013 C2H2-TYPE.
FT	DNA_BIND 2152 2211 HOMEBOX 1.
FT	DNA_BIND 2249 2308 HOMEBOX 2.
FT	ZN_FING 2335 2358 C2H2-TYPE (ATYPICAL).
FT	ZN_FING 2539 2561 C2H2-TYPE.
FT	DNA_BIND 2650 2709 HOMEBOX 3.
FT	ZN_FING 2720 2743 C2H2-TYPE.
FT	DNA_BIND 2952 3011 HOMEBOX 4.
FT	ZN_FING 3032 3056 C2H2-TYPE.
FT	ZN_FING 3552 3576 C2H2-TYPE.
FT	DOMAIN 461 491 POLY-GLU.
FT	DOMAIN 771 785 POLY-ALA.
FT	DOMAIN 1314 1317 POLY-ALA.
FT	DOMAIN 1734 1748 POLY-GLN.
FT	DOMAIN 1794 1799 POLY-GLN.
FT	DOMAIN 1856 1863 POLY-GLN.
FT	DOMAIN 2059 2059 POLY-PRO.
FT	DOMAIN 2405 2408 POLY-ALA.
FT	DOMAIN 3216 3220 POLY-PRO.
FT	DOMAIN 3380 3409 POLY-GLN.
FT	DOMAIN 3412 3420 POLY-GLN.
FT	DOMAIN 3534 3550 POLY-GLY.

FT DOMAIN 3620 3623 POLY-PRO.
FT DOMAIN 3659 3662 POLY-SER.
SQ SEQUENCE 3726 AA; 406567 MW; 915ACBE588A72C98 CRC64;

Query Match 6.8%; Score 84.5; DB 1; Length 3726;
Best Local Similarity 21.6%; Pred. No. 80; Mismatches 70; Indels 93; Gaps 12;
Matches 53; Conservative 29; Mismatches 70; Indels 93; Gaps 12;

QY 29 DCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDEE--LCGGLMRLVLAQRWMERL 86
Db 3033 ECTLCGIRKYSARLSVRDHIFSQOHISKVKDTIGSQLDKRKEKFFDPATVROQLMAQQLDRI 3092
QY 87 KTV-----AGSKMOGL-----LERVNTIEHYTKCAFO--PP-----PSCLEFVQTN 126
Db 3093 KKAENVIGLAAQQQGMFDNAPLQALNLP--TTPALQGIIPVLLPGLNRPSPJPGFTPAN 3149
QY 127 ISRLQETSEQLVALKPMITRONFSCRLELOCQPDSSITLPPPW-----S 170
Db 3150 TA-----LTSPKP-----NLMGLP-STIVPSGLPTSGLPNKPSASLSS 3188
QY 171 PRPLEATAPTAPOPPPLLLLLLPVGLLLAAAWCLHWQTRRRTPRPGEQVPP----- 223
Db 3189 PTPAQAATWAMAPPP-----PQPQOPQPPVQOPPPPPPAQO 3224
QY 224 VPSPO 228
Db 3225 IPAPQ 3229

Search completed: May 27, 2003, 18:27:34
Job time : 15 secs

Db 121 RFOVQNIHSLDQTSQQLAALKPWITRRNFSCLCQCPDSSSTLPPRSPALGATSL 180
 QY 181 APOPP-LLTLLLPVGLLLAAWCLHMORTRRRPPRPGEO-----POD 229
 Db 181 APOAPRLLTLLLPVALLLMSTAMCLHMWRRRRRRSPYGEQRTLRPSRSHLPED 236

RESULT 2

Q9M2U9 PRELIMINARY: PRT: 291 AA.
 ID 09M2U9
 AC 09M2U9
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Flt3 ligand.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20358731; PubMed=10902925;
 RA Yang S., Sim G.K.;
 RT "Molecular cloning of canine and feline flt3 ligand reveals high
 degree of similarity to the human and mouse homologue but uniquely
 long cytoplasmic domain."
 RL DNA Seq. 11:163-166(2000).
 DR EMBL; AF15149; AAF87089.1;
 DR InterPro: IPR004213; Flt3_119.
 DR Pfam: PF02947; flt3_119; 1.
 SO SEQUENCE 291 AA; 32459 MW; 8F85A10A5EADCC6 CRC64;

Query Match 72.0%; Score 894.5; DB 6; Length 291;
 Best Local Similarity 80.5%; Pred. No. 4.3e-80;
 Matches 178; Conservative 9; Mismatches 33; Indels 1; Gaps 1;

QY 1 MTVLAPAWSPTTLLTLLSSGLSGTDCSFQHSFPAVKIRELSDYLLQDYPVT 60
 Db 1 MIVLAPAWSPTTLLTLLSPGLSPDCSFHSFSTFVTRKLSDYLLQDYPVT 60
 QY 61 ASNLQDEELCGGLRLVLAQRMERLKTAVAGSKMGLERVTETHEFTVTKCAFOPPPSC 120
 Db 61 ASNLQDEELCGFVRLVLAQRMGRKLVAGSKMGLERVTETHEFTVTKCAFOPPL 120
 QY 121 RFOVQNIHSLQETSEQVLAALKPWITRRNFSCLCQCPDSSSTLPPRSPALGATAP 180
 Db 121 RFOVQNIHSLQDTSQQLAALKPWITRRNFSCLCQCPDSSSTLPPRSPALGATAP 180
 QY 181 APOPP-LLTLLLPVGLLLAAWCLHMORTRRRPPRPGEO 220
 Db 181 APOAPRLLTLLLPVALLLMSTAMCLHMWRRRRRRSPYGEQRTLRPSRSHLPED 221

RESULT 3

Q9GKEO PRELIMINARY: PRT: 292 AA.
 ID 09GKEO
 AC 09GKEO
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Flt3 ligand isoform-1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20570936; PubMed=11120823;
 RA Wang, W., Brown W.C., Palmer G.H.;
 RT "Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
 required for receptor binding and function using naturally occurring
 ligand isoforms.";

RL J. Immunol. 165:6966-6974(2000).
 DR EMBL; AF282985; AAF9322.1;
 DR InterPro: IPR004213; Flt3_119.
 DR Pfam: PF02947; flt3_119; 1.
 SO SEQUENCE 292 AA; 32390 MW; D6B9ED79221202D CRC64;

Query Match 67.6%; Score 840; DB 6; Length 292;
 Best Local Similarity 76.3%; Pred. No. 1e-74;
 Matches 171; Conservative 12; Mismatches 37; Indels 4; Gaps 2;

QY 1 MTVLAPAWSPTT-YLLTLLSSGLSGTDCSFQHSFPAVKIRELSDYLLQDYPVT 59
 Db 1 MIVLAPAWSPTTSLTLLSPGLSPDCSFHSFSTFVTRKLSDYLLQDYPVT 60
 QY 60 VASNLQDEELCGGLRLVLAQRMERLKTAVAGSKMGLERVTETHEFTVTKCAFOPPPSC 119
 Db 61 VASNLQDDKLCGAFVRLVLAQRMGRKLVAGSEMEKLEEDVTETHEFTVTKCAFOPPL 120
 QY 120 LRFVQNIHSLQETSEQVLAALKPWITRRNFSCLCQCPDSSSTLPPRSPALGATAP 179
 Db 121 LRFVQNIHSLQDTHQQLAALKPWITRRNFSCLCQCPDSSSTLPPRSPALGATSL 180
 QY 180 TAPOPP-LLTLLLPVGLLLAAWCLHMORTRRRPPRPGEO 220
 Db 181 PGPQSPLLTLLLPVALLLMSTAMCLHMWRRRRRRTRYPGER 224

RESULT 4

Q8WNM1 PRELIMINARY: PRT: 292 AA.
 ID 08WNM1
 AC 08WNM1
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Flt3 ligand.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hikono H., Momotani E.;
 RT "Cloning of a cDNA for bovine flt3 ligand."
 RT Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB051841; BAB79634.1;
 DR InterPro: IPR004213; Flt3_119.
 DR Pfam: PF02947; flt3_119; 1.
 SO SEQUENCE 292 AA; 32388 MW; 2A797E0C1199C1D9 CRC64;

Query Match 67.2%; Score 835; DB 6; Length 292;
 Best Local Similarity 75.9%; Pred. No. 3.2e-74;
 Matches 170; Conservative 12; Mismatches 38; Indels 4; Gaps 2;

QY 1 MTVLAPAWSPTT-YLLTLLSSGLSGTDCSFQHSFPAVKIRELSDYLLQDYPVT 59
 Db 1 MIVLAPAWSPTTSLTLLSPGLSPDCSFHSFSTFVTRKLSDYLLQDYPVT 60
 QY 60 VASNLQDEELCGGLRLVLAQRMERLKTAVAGSKMGLERVTETHEFTVTKCAFOPPPSC 119
 Db 61 VASNLQDDKLCGAFVRLVLAQRMGRKLVAGSEMEKLEEDVTETHEFTVTKCAFOPPL 120
 QY 120 LRFVQNIHSLQETSEQVLAALKPWITRRNFSCLCQCPDSSSTLPPRSPALGATAP 179
 Db 121 LRFVQNIHSLQDTHQQLAALKPWITRRNFSCLCQCPDSSSTLPPRSPALGATSL 180
 QY 180 TAPOPP-LLTLLLPVGLLLAAWCLHMORTRRRPPRPGEO 220
 Db 181 PGPQSPLLTLLLPVALLLMSTAMCLHMWRRRRRRTRYPGER 224

RESULT 5

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09GKD9
ID 09GKD9 PRELIMINARY: PRT: 274 AA.
AC 09GKD9;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Flt3 ligand isoform-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20570936; PubMed=11120823;
RA Wang J. W., Brown W. C., Palmer G. H.;
RT Identification of fetal liver tyrosine kinase 3 (Flt3) ligand domain
RT required for receptor binding and function using naturally occurring
RT ligand isoforms.
RL J. Immunol. 165:6966-6974(2000).
DR EMBL: AF282986; AAF99323.1;
DR InterPro: IPR004213; Flt3_1lg.
DR Pfam: PF02947; flt3_1lg.1
SQ SEQUENCE 274 AA; 30372 MW; 725A7F77A95DA98B CRC64;

Query Match
Best Local Similarity 60.1%; Score 746; DB 6; Length 274;
Matches 156; Conservative 12; Mismatches 34; Indels 22; Gaps 3;

OY 1 MTVLAPAMSP-PTT-YLLLLLLLSSGSGTODCSFQHSPISSDFAVKIRELSDYLLDYPVT 59
DB 1 MTVLAPAMSPPTSLLLLLLLLSPGLGTPDCSFRHSPISSSTFAIKIKLSKYLLDYPVT 60
OY 60 VASNLDEELCGGLMRLVLAORMERLKTVAAGSKMOGLERVNTETHEVTKCAFQPPSC 119
DB 61 VASNLDDDLKCGAFMLVLAORMGSLKTYAGSEMEKLEVDVTEHFVSCAF----- 114
OY 120 LRFVOTNISRLQETSQOLVALKPWITRNFSCLELQCPDPSSTLPPSPRPLEATAP 179
DB 115 -----QDTHQGEALKPWITRNFSCLELQCPDPSSTLPPSPRPLEATAP 162
OY 180 TAPQPP-----LFLLLLPVGLLLLAAMCLHMOTRRTRPPRQCO 220
DB 163 PGPSPPLLLLLLLLPVALLLATAWCLCRMRRRRRTRPPR 206

RESULT 6
061104
ID 061104 PRELIMINARY: PRT: 172 AA.
AC 061104;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Flt3 ligand, T169 form.
GN Flt3L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA McClanahan T., Culpepper J., Campbell D., Wagner J., Franz-Bacon K.,
RA Matsson J., Tsai S., Loh J., Guimares M. J., Matzel M. G., Rosnet O.,
RA Birnbaum D., Hannum C.;
RT "Flt3 ligand: expression, genomic organization, alternatively spliced
RT forms and processing."
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
DE Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL: U44024; AAG3305.1;
DR MGD: MGI:95560; Flt3l.
DR InterPro: IPR004213; Flt3_1lg.
DR Pfam: PF02947; flt3_1lg.1
DR PROSITE: PS00294; PRENITATION; UNKNOWN_1.

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SQ SEQUENCE 172 AA; 19465 MW; 04F0A01017E3384 CRC64;

Query Match
Best Local Similarity 48.5%; Score 602.5; DB 11; Length 172;
Matches 122; Conservative 15; Mismatches 28; Indels 3; Gaps 2;

OY 1 MTVLAPAMSP-PTT-YLLLLLLLSSGSGTODCSFQHSPISSDFAVKIRELSDYLLDYPVT 59
DB 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVFRFETDHLKDYPT 60
OY 60 VASNLDEELCGGLMRLVLAORMERLKTVAAGSKMOGLERVNTETHEVTKCAFQPPSC 119
DB 61 VAVNLDEKHKALMSLFLAORMIQTLTVAGSKMOTLEVDVTEHFVSCFQPLPEC 120
OY 120 LRFVOTNISRLQETSQOLVALKPWITR--QNFSCLELQCPDPSSTLPPSPR 165
DB 121 LRFVOTNISRLKDTCTQLLALPKPCIGKACQNFSCLEVQCPDPSVSL 168

RESULT 7
08VCH4
ID 08VCH4 PRELIMINARY: PRT: 169 AA.
AC 08VCH4;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to FMS-like tyrosine kinase 3 ligand.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Straussberg R.;
RA TISSUE=LIVER;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC019801; AAH19801.1;
DR InterPro: IPR004213; Flt3_1lg.
DR Pfam: PF02947; flt3_1lg.1.
DR KINASE.
SQ SEQUENCE 169 AA; 18986 MW; 5B4CA47D9724EFF2 CRC64;

Query Match
Best Local Similarity 46.5%; Score 578; DB 11; Length 169;
Matches 120; Conservative 14; Mismatches 29; Indels 12; Gaps 3;

OY 1 MTVLAPAMSP-PTT-YLLLLLLLSSGSGTODCSFQHSPISSDFAVKIRELSDYLLDYPVT 59
DB 1 MTVLAPAMSPNSLLLLLLLSPCLRGTPDCYFSHSPISSNFKVFRFETDHLKDYPT 60
OY 60 VASNLDEELCGGLMRLVLAORMERLKTVAAGSKMOGLERVNTETHEVTKCAFQPPSC 119
DB 61 VAVNLDEKHKALMSLFLAORMIQTLTVAGSKMOTLEVDVTEHFVSCFQPLPEC 120
OY 120 LRFVOTNISRLQETSQOLVALKPWITR--QNFSCLELQCPDPSSTLPPSPR 172
DB 121 LRFVOTNISRLKDTCTQLLALPKPCIGKACQNFSCLELQCPDPSVSL 166

RESULT 8
09LG68
ID 09LG68 PRELIMINARY: PRT: 579 AA.
AC 09LG68;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative extensin-like protein.
GN P0406H10.6 OR O1174_D05.5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;

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RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, PAC
 clone: P040610."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, BAC
 clone: O11174_D05."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP002524; BAB07956.1;
 DR EMBL: AP003118; BAB33013.1;
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003592; LRR_out.
 DR InterPro: IPR002965; P_tich_extensn.
 DR InterPro: IPR003504; RNA_rec_mot.
 DR Pfam: PF00560; LRR; 6.
 DR PRINTS: PRO1582; KV33CHANNEL.
 DR PRINTS: PRO1217; PRICHEXTENSIN.
 DR SMART: SM00370; LRR; 5.
 DR PROSITE: PS00030; RRM_RNP_1; UNKNOWN_1.
 SQ SEQUENCE 579 AA; 62607 MW; 04457E18E7405AFAF CRC64;

Query Match 9.1%; Score 112.5; DB 10; Length 579;
 Best Local Similarity 23.7%; Pred. No. 0.013;
 Matches 54; Conservative 28; Mismatches 69; Indels 77; Gaps 11;

QY 17 LLLLSGLSGTDCSPHSPFSSDPFAVKIRELSDYLLQDYPTVASNLQDELGGIMRL 76
 DB 244 ILINIGLS-----SCLPEVGM-LREYVVF-----DVSPNRLAGPLPSA 282
 QY 77 VLAQRMWERLKTAVGSKMOGLERVNTFHFVTKCAFO-----PPSCARFV-----QT 125
 DB 283 VAGMKVEQL-DVAHNLGALIQAVCELPRLNFTFAVNETGPEPSCAHAVPRYGRDR 341
 QY 126 NI--SRLLQETSQALVALPMTWITRQNFNR-----CLELQCPDSSSTLPSPPLLEXTAP 179
 DB 342 NCLPNRPAGRTLRQCAAF-----FARPVNCAAFQCKPFYPALPPSPPP--SPP 391
 QY 180 TAQPPPLLLLLLPGVLLLLAAMCLHMQRTRRTTRPGEQVPPVSP 227
 DB 392 PSPPP-----SPPSPSTSPPPSP 411

RESULT 9

QY 09GY11 PRELIMINARY; PRT; 668 AA.
 AC 09GY11;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Probable surface antigen p2.
 GN LM12.156.
 OS Leishmania major.
 OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
 OLIVER K.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL390114; CAC02038.2;
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR002965; P_tich_extensn.
 DR Pfam: PF00560; LRR; 6.
 DR PRINTS: PRO1217; PRICHEXTENSIN.
 DR SMART: SM0181; EGF; 1.

SQ SEQUENCE 668 AA; 70725 MW; CEB3ECAAAC490C94 CRC64;

Query Match 8.4%; Score 104.5; DB 5; Length 668;
 Best Local Similarity 26.6%; Pred. No. 0.093;
 Matches 63; Conservative 20; Mismatches 77; Indels 77; Gaps 13;

QY 4 LAPAMSPPTTYLLLLLSGLSGTDCSPHSPFSSDPFAVKIRELSDYLLQDYPTVASN 63
 DB 149 LPPESSMPNLNQLQVRLKLSGT-----LPADMS-SKLSISNVLEDMPT----- 194
 QY 64 LQDELGGIMRLVLAQRMWERLKTAVGSKMOGLERVNTFHFVTKCAFOPP-----S 118
 DB 195 -----GL-----LPPEW-----GSLERIQQLVRLKLTGPILPQWSPMK 229
 QY 119 CLRFVQ---TNISRLQ-----ETSEQLVALKP-WITRQNFSCLELQCP 160
 DB 230 ALRFLLTLDGTLNLSGLTPPQWSAMASVLSLNEGTEVSGTLPPKVISMSRL-QTLNLRRTK 288
 QY 161 DSSTLPPEWSPR-----PLEATAPTAPOP-----LLLLLLPVGLL--LLAAAW 203
 DB 289 VSGTLPPPEWSSMSLANLQSLTGVSGTLPPQWSMKRLTQLLLTDLTSLGTLPAEW 345

RESULT 10

QY 09GY33 PRELIMINARY; PRT; 648 AA.
 AC 09GY33;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Probable surface antigen p2.
 GN LM12.121.
 OS Leishmania major.
 OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRIEDLIN;
 RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.,
 OLIVER K.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL390114; CAC02017.2;
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR002965; P_tich_extensn.
 DR Pfam: PF00560; LRR; 7.
 DR PRINTS: PRO1217; PRICHEXTENSIN.
 DR SMART: SM00181; EGF; 1.
 SQ SEQUENCE 648 AA; 68470 MW; 8EB78AC101E01286 CRC64;

Query Match 8.3%; Score 102.5; DB 5; Length 648;
 Best Local Similarity 26.6%; Pred. No. 0.14; 77; Indels 77; Gaps 13;

QY 4 LAPAMSPPTTYLLLLLSGLSGTDCSPHSPFSSDPFAVKIRELSDYLLQDYPTVASN 63
 DB 149 LPPESSMPNLNQLQVRLKLSGT-----LPADMS-SKLSISNVLEDMPT----- 194
 QY 64 LQDELGGIMRLVLAQRMWERLKTAVGSKMOGLERVNTFHFVTKCAFOPP-----S 118
 DB 195 -----GL-----LPPEW-----GSLERIQQLVRLKLTGPILPQWSPMK 229
 QY 119 CLRFVQ---TNISRLQ-----ETSEQLVALKP-WITRQNFSCLELQCP 160
 DB 230 ALRFLLTLDGTLNLSGLTPPQWSAMASVLSLNEGTEVSGTLPPKVISMSRL-QTLNLRRTK 288
 QY 161 DSSTLPPEWSPR-----PLEATAPTAPOP-----LLLLLLPVGLL--LLAAAW 203
 DB 289 VSGTLPPPEWSSMSLANLQSLTGVSGTLPPQWSMKRLTQLLLTDLTSLGTLPAEW 345

RESULT 11

OBVIM6

ID 08VIM6 PRELIMINARY: PRT: 1809 AA.
AC 08VIM6;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 21, Last annotation update)
DE Stereocilin.
GN STRC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RX MEDLINE=21547528; PubMed=11687802;
RA Verpy E., Masmodi S., Zwaenepoel I., Leiboldi M., Hutchin T.P.,
RA Del Castillo I., Nouaille S., Blanchard S., Laine S., Popot J.L.,
RA Moreno F., Mueller R.F., Petit C.;
RT "Mutations in a new gene encoding a protein of the hair bundle cause
RT non-syndromic deafness at the DFNB16 locus."
RL Nat. Genet. 29:345-349 (2001).
DR EMBL; AF375593; AAL35321.1;
DR MGD; MGI:2153816; Strc.
SQ SEQUENCE 1809 AA; 196404 MM; 012382C9E80EC825 CRC64;

Query Match
Best Local Similarity 23.7%; Score 100.5; DB 11; Length 1809;
Matches 70; Conservative 25; Mismatches 93; Indels 107; Gaps 14;

QY 3 VLAPASPTTYLL-----LLLL-----SSGLSGQDCSFQHSPISSDPAVKIRE 47
DB 168 VLADLPLSLMLLEGTMOALVOLQPSVDPINATGLDG-----RE 208
QY 48 LSDYLLQDY--PYTVASNLQDEE-LCGLMRLV---LAQRMERLKV----- 89
DB 209 PAHFQGLGLITPAGELGSEBALMGGLRTYGAPLYAFOGSLRVTSLQDEVSIM 268
QY 90 -----AGSKMGLLEVRNTEIHFVTKC-----AFQPPSCLRFVQNTISRL 131
DB 269 GQEPDASGCGGNGQLLQMLMGRNNLSMDARALGFLSGPPPPALLCLSGV--L 326
QY 132 QETSEGLVAKWITRQNSRCLQCCPDSSLLP-----PWSPPLE 175
DB 327 PRASQPAHISF--RQRAISVEALCENHSGEPEYSISNFYLLQHIKIPATPRPP 383
QY 176 AT---APTAPPLLLLLLPVGLLLAAMCLHMQRTRRRPRGQV--PPPS 226
DB 384 TTPRPPTTPQPPPTTTPP-----DTTQPPVTPRPPPTTPPPPS 426

RESULT 12
Q9N753
ID 09N753 PRELIMINARY: PRT: 345 AA.
AC 09N753;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Probable surface antigen p2.
GN IM2.08.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OC NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Bartell B.,
RA Oliver K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL390114; CAB98658.2;
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR Pfam; PF00560; LRR_3.
DR SMART; SM00370; LRR_3.

SQ SEQUENCE 345 AA; 37530 MM; 06ECC50B1B54B70 CRC64;
Query Match
Best Local Similarity 7.9%; Score 98.5; DB 5; Length 345;
Matches 56; Conservative 21; Mismatches 57; Indels 101; Gaps 10;

QY 6 PAWSPTTYLLLLLLSSGSGT-----QDCSFQHSPISSDPAVKIRELS 49
DB 152 PEMGWSLTSVNLKGTGTSGTLPPQWSGMSKARLQDDCLDGLSGLSFSSMSAI----- 205
QY 50 DYLLQDYPTVAVASNLQDEELCG-----GLMRLVLAQRMERLKVAGSKMGLLEVRNTE 104
DB 206 -----PMLASVSLAKNKKFCVCRTGRRLVLL--WTSKISTRATA----- 245
QY 105 IHFVTKAFQF---PPSCIRFVQNTISRLQETSQVLALEKWTTRQNSRCLQCCPD 161
DB 246 --WLRTRQRPPLSPPPQRPRTSLT-----FPLRRGR 278
QY 162 SSTLPSPSPRLTAPAPQPLLLL---LLPVGLLLAAMCLHMQRTR 212
DB 279 LSRLLQPALRRLN-----PQPLRRLNRPRLP-----QQTR 313

RESULT 13
Q9DWH8
ID 09DWH8 PRELIMINARY: PRT: 1240 AA.
AC 09DWH8;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Pz.
GN R2.
OS Rat cytomegalovirus (strain Mastricht).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
OC NCBI_TaxID=79700;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MASTRICHT;
RX MEDLINE=20366325; PubMed=10906222;
RA Vink C., Beuken E., Bruggeman C.A.;
RT "Complete DNA sequence of the rat cytomegalovirus genome."
RL J. Virol. 74:7656-7665 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MASTRICHT;
RX MEDLINE=20473137; PubMed=11018281;
RA Grulithuisen Y.K., Beuken E., Bruggeman C.A., Vink C.;
RT "Rat cytomegalovirus R89 is a highly conserved gene which expresses a
RT spliced transcript."
RL Virus Res. 69:119-130 (2000).
DR EMBL; AF232689; AAF99111.1;
DR SEQUENCE 1240 AA; 125612 MM; 33B6C13DC6A272B0 CRC64;

Query Match
Best Local Similarity 7.7%; Score 95.5; DB 12; Length 1240;
Matches 29; Conservative 8; Mismatches 18; Indels 33; Gaps 5;

QY 160 PDSSSTL-----PPWSRP--LEATAPAPQ-PLLLLLLPVGLLLAA 201
DB 1060 PDSTAVTGATTERSPATEPRPRRPLPGVSAPLAPQPTLLSLVPA----- 1112
QY 202 AMCLHMQRTRRRTPRPGQVPPVPSPD 229
DB 1113 -----QATRASPPRETDAF-PTPAD 1132

RESULT 14
Q9C5T0
ID 09C5T0 PRELIMINARY: PRT: 658 AA.
AC 09C5T0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

GenCore version 5.1.4-p5-4578
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OW protein - protein search, using sw model

Run on: May 27, 2003, 18:24:51 ; Search time 36 seconds
(without alignments)
869,830 Million cell updates/sec

Title: US-08-994-468-6
Perfect score: 1242
Sequence: 1 MVLAPAWSPFTYLLLL... REGEVPPVPSDDILVER 235

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

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23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length DB	ID	Description
1	1242	100.0	235	16 AAR67541	Human flt-3 ligand
2	1242	100.0	235	20 AAM67769	Human flt3-1ligand
3	1242	100.0	235	21 AAY69719	Full length wild t
4	1242	100.0	235	22 AAB20192	Human flt-3 ligand
5	1242	100.0	235	23 ABB08129	Human flt3b polype
6	1236	99.5	235	16 AAR66175	Human S86/S109 flt
7	1236	99.5	235	22 AAB20194	Human flt-3 ligand
8	1124	90.5	212	21 AAY69721	Human flt-3 mutein
9	1114	89.7	209	19 AAM69007	Human flt-3 recept
10	1114	89.7	209	21 AAY69720	Mature wild type h

11	1110	89.4	209	21 AAY69723	Human flt-3 mutein
12	1110	89.4	209	21 AAY69726	Human flt-3 mutein
13	1110	89.4	209	21 AAY69727	Human flt-3 mutein
14	1110	89.4	209	21 AAY69729	Human flt-3 mutein
15	1108	89.2	209	21 AAY69722	Human flt-3 mutein
16	1108	89.2	209	21 AAY69724	Human flt-3 mutein
17	1107	89.1	209	21 AAY69728	Human flt-3 mutein
18	1100	88.6	209	21 AAY69725	Human flt-3 mutein
19	970	78.1	185	22 AAB20195	Human flt-3 ligand
20	895.5	72.1	294	21 AAY58204	Canine flt-3 ligand
21	894.5	72.0	291	21 AAY58210	Feline flt-3 ligand
22	834	67.1	178	22 AAB20193	Human flt-3 ligand
23	797.5	64.2	268	21 AAY58206	Canine mature flt-
24	796.5	64.1	276	21 AAY58207	Canine mature flt-
25	791.5	63.7	265	21 AAY58211	Feline mature flt-
26	768.5	61.9	231	16 AAR67540	Mouse flt-3 ligand
27	768.5	61.9	231	20 AAM67768	Mouse flt-3 ligand
28	768.5	61.9	231	22 AAB20186	Mouse flt-3 ligand
29	768	61.8	232	16 AAR66177	Mouse flt-3 ligand
30	764	61.5	232	22 AAB20189	Mouse flt-3 ligand
31	745	60.0	150	19 AAM67930	Human flt-3 recept
32	745	60.0	150	19 AAM69054	Human flt-3 recept
33	740.5	59.6	377	19 AAM78124	Human flt-3 recept
34	739	59.5	143	19 AAM77926	Human flt-3 recept
35	739	59.5	143	19 AAM69050	Human flt-3 recept
36	737.5	59.4	349	19 AAM63289	Human flt-3 recept
37	737.5	59.4	349	19 AAM78005	Human flt-3 recept
38	736.5	59.3	340	19 AAM63291	Human flt-3 recept
39	736.5	59.3	349	19 AAM63286	Human flt-3 recept
40	736.5	59.3	523	19 AAM78008	Human flt-3 recept
41	735	59.2	140	19 AAM77911	Human flt-3 recept
42	735	59.2	140	19 AAM69035	Human flt-3 recept
43	735	59.2	144	19 AAM77928	Human flt-3 recept
44	735	59.2	144	19 AAM69052	Human flt-3 recept
45	735	59.2	313	19 AAM63294	Human flt-3 recept

ALIGNMENTS

RESULT 1
ID AAR67541 standard; protein: 235 AA.

XX AC AAR67541;
XX 05-AUG-1995 (first entry)
XX DE Human flt-3 ligand.

XX KW flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.

XX OS Homo sapiens.

XX PH Key
XX FT Peptide
XX FT Location/Qualifiers
XX FT 1..26
XX FT /note="Sig peptide
XX FT /note="signal peptide may extend to position 27"

XX FT Domain
XX FT 27..182
XX FT /label="Extracellular domain
XX FT /note="extracellular domain may start at position 28"

XX FT Domain
XX FT 183..205
XX FT /label="Transmembrane domain
XX FT 206..235
XX FT /label="Cytoplasmic domain

XX PN EP627487-A.

XX PD 07-DEC-1994.

XX PF 19-MAY-1994; 94EP-0303575.

XX

PR 24-MAY-1993; 93US-0068394.
 PR 12-AUG-1993; 93US-0106463.
 PR 25-AUG-1993; 93US-0111758.
 PR 03-DEC-1993; 93US-0162407.
 PR 07-MAR-1994; 94US-0209502.
 PR 11-MAY-1994; 94US-0243545.
 XX
 PA (IMMUNEX) IMMUNEX CORP.
 XX
 PI Beckmann MP, Lyman SD;
 XX
 DR WPI: 1995-008071/02.
 DR N-PSDB: AA079079.
 XX
 PT Isolated ligands for flt 3 receptors - useful for treating
 XX anemias, AIDS and various cancers
 XX
 PS Disclosure: Page 29-30; 33pp; English.
 XX
 CC A human T-cell lambda-gli0 random primed cDNA library was
 CC screened with a fragment corresponding to the extracellular
 CC domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AA079076)
 CC to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and
 CC stem cells, and can be used e.g. in gene therapy protocols.
 CC
 XX
 SQ Sequence 235 AA;
 Query Match 100.0%; Score 1242; DB 16; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLAPAMSPPTTYLLLLSSGSLGCTODCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
 DB 1 MTVLAPAMSPPTTYLLLLSSGSLGCTODCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
 QY 61 ASNLODEELCGGLMRLVLAQRMMERLKTAVAGSKMGLLEVRNTEIHFTVKCAFQPPPSCL 120
 DB 61 ASNLODEELCGGLMRLVLAQRMMERLKTAVAGSKMGLLEVRNTEIHFTVKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPWPMSPRELEATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPWPMSPRELEATAPT 180
 QY 181 APOPLLILLLPVGLLLAAACLMQRTRRTPRPGEOVPVPSPDQLLVEH 235
 DB 181 APOPLLILLLPVGLLLAAACLMQRTRRTPRPGEOVPVPSPDQLLVEH 235
 RESULT 2
 AA67769
 ID AA67769 standard; Protein: 235 AA.
 AC AA67769;
 DT 25-MAR-1999 (first entry)
 DE Human flt3-ligand.
 DE
 XX Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;
 KM immunogenic; autoimmune disease; organ transplantation; food allergy;
 KM tissue transplantation.
 OS Homo sapiens.
 XX
 PN W09857655-A1.
 XX
 PD 23-DEC-1998.
 XX
 PF 12-JUN-1998; 98MO-US12085.
 XX
 PR 17-JUN-1997; 97US-0877421.
 XX
 PA (IMMUNEX) IMMUNEX CORP.

XX
 PI Abbott NM, Mowat AM, Viney JL;
 XX
 DR WPI: 1999-070422/06.
 DR N-PSDB: AA81506.
 XX
 PT Methods for initiating or enhancing antigen specific immune
 PT tolerance - by using murine or human flt3 ligand
 XX
 PS Claim 1: Page 14-15; 25pp; English.
 XX
 CC A method has been developed of initiating or enhancing: (i) an antigen-
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic
 CC immunogenic molecule by addition of a polypeptide, before, after or with
 CC the mucosal administration of an immunotolerizing amount of the antigen
 CC or therapeutic molecule, respectively. The polypeptide is capable of
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino
 CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;
 CC and c) a polypeptide that has at least 90% identity to the polypeptides
 CC of either (a) or (b). The method ameliorates the effects of autoimmune
 CC diseases, food allergies or organ or tissue rejection following
 CC transplantation. Administration of flt3-L allows lower doses of antigens
 CC to be used in vivo for mucosally administered antigens. The present
 CC sequence represents human flt3-L.
 CC
 XX
 SQ Sequence 235 AA;
 Query Match 100.0%; Score 1242; DB 20; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVLAPAMSPPTTYLLLLSSGSLGCTODCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
 DB 1 MTVLAPAMSPPTTYLLLLSSGSLGCTODCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
 QY 61 ASNLODEELCGGLMRLVLAQRMMERLKTAVAGSKMGLLEVRNTEIHFTVKCAFQPPPSCL 120
 DB 61 ASNLODEELCGGLMRLVLAQRMMERLKTAVAGSKMGLLEVRNTEIHFTVKCAFQPPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPWPMSPRELEATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQLQCPDSSSTLPWPMSPRELEATAPT 180
 QY 181 APOPLLILLLPVGLLLAAACLMQRTRRTPRPGEOVPVPSPDQLLVEH 235
 DB 181 APOPLLILLLPVGLLLAAACLMQRTRRTPRPGEOVPVPSPDQLLVEH 235
 RESULT 3
 AA69719
 ID AA69719 standard; Protein: 235 AA.
 AC AA69719;
 DT 05-JUL-2000 (first entry)
 DE Full length wild type human flt-3 protein.
 DE
 XX Immunomodulator; immunosuppressive; cytostatic; antineoplastic; anti-HIV;
 KM neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 KM cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KM cellular expansion; cellular differentiation; natural killer cell;
 KM cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KM myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KM multiple myeloma; leukemia.
 XX
 OS Homo sapiens.
 XX
 PN W0200001823-A2.
 XX
 PD 13-JAN-2000.

PF 25-JUN-1999; 99WO-US14296.
 XX 02-JUL-1998; 98US-0109100.
 XX (IMMUNEX CORP.
 PA Graddis TJ, McGrew JT;
 XX WPI, 2000-182115/16.
 DR N-PSDB; AA259064.
 XX
 PT Mutant soluble Flt-3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122
 XX
 PS Claim 1: Page 72-73; 90pp; English.
 XX
 CC The invention relates to novel soluble Flt-3 ligand (Flt-3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (this sequence) or mature (AA60720) Flt-3-L
 CC polypeptides. The Flt-3-L protein binds cell surface tyrosine kinase
 CC receptors and regulate growth and differentiation of hematopoietic
 CC progenitor cells. The Flt-3-L protein can be used to induce cellular
 CC hematopoietic, natural killer (NK) or dendritic cells, especially in the
 CC presence of growth factors such as interleukins, colony stimulating
 CC factors or protein kinases. The protein can also modulate, augment or
 CC enhance a patient's immune response and can be used to treat an immune
 CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
 CC may be used to treat a pathological condition e.g. myelodysplasia,
 CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
 CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
 CC leukemia.
 CC
 SO Sequence 235 AA:
 Query Match 100.0%; Score 1242; DB 21; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVALPAMSPPTTYLLLLLSGLSGTODCSFQHSPTSSDFAVKIRELSYLLQDVPVY 60
 DB 1 MTVALPAMSPPTTYLLLLLSGLSGTODCSFQHSPTSSDFAVKIRELSYLLQDVPVY 60
 QY 61 ASNLODEELCGGLWRLVLAQRMRERLKTVAAGSKMGLLERVNTIEHFVTKCAFQPPSCL 120
 DB 61 ASNLODEELCGGLWRLVLAQRMRERLKTVAAGSKMGLLERVNTIEHFVTKCAFQPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPMPSPRLATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPMPSPRLATAPT 180
 QY 181 APQPPPLLILLPVGLLLAAAMCLHMORTRRRTPRGQVPPVPEODLLVEH 235
 DB 181 APQPPPLLILLPVGLLLAAAMCLHMORTRRRTPRGQVPPVPEODLLVEH 235
 RESULT 4
 ID AAB20192 standard; Protein: 235 AA.
 XX
 AC AAB20192;
 XX
 DT 14-MAY-2001 (first entry)
 XX
 DE Human Flt-3 ligand.
 XX
 KM Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
 KM immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KM lymphoma; autoimmune disease; infection; gene therapy;
 OS Homo sapiens.
 XX

FH Key Location/Qualifiers
 FT Peptide 1..26
 FT Protein /label- signal_peptide
 FT Protein 27..235
 FT Domain /label- Mature-protein
 FT Domain 27..182
 FT Domain /label- Extracellular_domain
 FT Domain 183..205
 FT Domain /label- Transmembrane_domain
 FT Domain 206..235
 FT Domain /label- Cytoplasmic_domain
 PN W0200109303-A2.
 XX
 PD 08-FEB-2001.
 XX
 PF 31-JUL-2000; 2000WO-US20679.
 XX
 PR 30-JUL-1999; 99US-0146170.
 XX
 PA (VICA-) VICAL INC.
 XX
 PI Hermanson GG;
 DR WPI, 2001-123319/13.
 DR N-PSDB; AAF30310.
 XX
 PT Immunogenic compositions comprising Flt-3 ligand encoding
 PT polynucleotide and one or more antigen, or cytokine encoding
 PT polynucleotides, useful for suppressing tumour growth and for treating
 PT autoimmune diseases (e.g. rheumatoid arthritis)
 XX
 PS Claim 2: Page 132-133; 149pp; English.
 XX
 CC The present sequence is that of human Fms-like tyrosine kinase
 CC (Flt-3 ligand). The invention is directed to enhancing the
 CC immune response of a vertebrate to an antigen or a cytokine by
 CC administering in vivo, into a tissue of a vertebrate, a Flt-3
 CC ligand-encoding polynucleotide, and 1 or more antigen- or
 CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
 CC polynucleotide may encode the present full-length human Flt-3
 CC ligand polypeptide, or amino acids 27-160, 1-160, 27-185, 1-185,
 CC or 27-235 of the ligand. The polynucleotides are incorporated
 CC into the cells of the vertebrate in vivo, and a prophylactically
 CC or therapeutically effective amount of Flt-3 ligand and 1 or more
 CC antigens or cytokines is produced in vivo. Pharmaceutical
 CC compositions comprising the polynucleotides are useful for
 CC suppressing tumour growth in a mammal. The tumour is melanoma,
 CC glioma or lymphoma, particularly B-cell lymphoma. They can also
 CC be used for the prophylactic and/or therapeutic treatment of:
 CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
 CC and C in humans), parasitic (e.g. malaria) and fungal infections;
 CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
 CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
 CC Various other examples of these diseases are given in the
 CC specification.
 CC
 SO Sequence 235 AA:
 Query Match 100.0%; Score 1242; DB 22; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTVALPAMSPPTTYLLLLLSGLSGTODCSFQHSPTSSDFAVKIRELSYLLQDVPVY 60
 DB 1 MTVALPAMSPPTTYLLLLLSGLSGTODCSFQHSPTSSDFAVKIRELSYLLQDVPVY 60
 QY 61 ASNLODEELCGGLWRLVLAQRMRERLKTVAAGSKMGLLERVNTIEHFVTKCAFQPPSCL 120
 DB 61 ASNLODEELCGGLWRLVLAQRMRERLKTVAAGSKMGLLERVNTIEHFVTKCAFQPPSCL 120
 QY 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPMPSPRLATAPT 180
 DB 121 RFVQTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPMPSPRLATAPT 180

DB 121 REVQTNISRLQETSDQVLAALKPWITRONFSRCLQCPDSSSTLPSPMSPRELEATAPT 180
 QY 181 AQPPLLLLLLPLVGLLLAAACLMHQMORTRRTPRPGQVPPVPSQDILLVEH 235
 DB 181 AQPPLLLLLLPLVGLLLAAACLMHQMORTRRTPRPGQVPPVPSQDILLVEH 235

RESULT 5

ABR08129 standard; protein; 235 AA.

ABR08129;

10-SEP-2002 (first entry)

Human Flt3L polypeptide.

Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;
 fungicide; protozoacide; virucide; anti-inflammatory; anti-HIV;
 tuberculostatic; cytostatic; human; Flt3L.

Homo sapiens.

WO200236141-A2.

10-MAY-2002.

30-OCT-2001; 2001WO-US44834.

02-NOV-2000; 2000US-245721P.

(IMMUNEX CORP.

Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE,
 Thomas EK;

WPI; 2002-500114/53.

Treating an individual suffering from infection, e.g. inflammation,
 chickenpox or AIDS, by administering a combination of dendritic cell
 mobilization factor or maturation agent, T cell enhancing factor and
 antigen-specific T cells -

Disclosure; Page 37-38; 43pp; English

The invention relates to treating an individual at risk for or suffering
 from infection with a pathogenic or opportunistic organism. The method
 involves administering a combination of two to five agents comprising:
 (a) dendritic cell mobilisation factor; (b) dendritic cell maturation
 agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;
 or (e) activated, antigen-specific T cells. The methods are useful for
 treating an individual at risk for or suffering from infection with a
 pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria
 (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.
 T. cruzi, which causes Chagas disease). The methods are especially
 useful for treating an individual suffering from immunosuppression by
 enhancing a lymphocyte-mediated immune response. In particular, the
 method is useful for treating inflammation, chickenpox, oral or genital
 herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS,
 T cell leukemia or T cell lymphoma. The activated antigen-presenting
 dendritic cells are useful as a vaccine adjuvant. The present sequence
 represents a human Flt3L polypeptide fragment, that can be used as a
 dendritic cell mobilisation factor.

Sequence 235 AA:

Query Match 100.0%; Score 1242; DB 23; Length 235;
 Best Local Similarity 100.0%; Pred. No. 5e-109;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYTLPAMSTPTLLLLLSGLSGTDCSFGHSPISDFAVKIRLSDYLQDVFVTV 60
 DB 1 MYTLPAMSTPTLLLLLSGLSGTDCSFGHSPISDFAVKIRLSDYLQDVFVTV 60

QY 61 ASNLODEELCGGLMRVLYLAORMMERLKTVAQSKMGLLEBVENIEIHFVTCAPQPPSCL 120
 DB 61 ASNLODEELCGGLMRVLYLAORMMERLKTVAQSKMGLLEBVENIEIHFVTCAPQPPSCL 120
 QY 121 REVQTNISRLQETSDQVLAALKPWITRONFSRCLQCPDSSSTLPSPMSPRELEATAPT 180
 DB 121 REVQTNISRLQETSDQVLAALKPWITRONFSRCLQCPDSSSTLPSPMSPRELEATAPT 180
 QY 181 AQPPLLLLLLPLVGLLLAAACLMHQMORTRRTPRPGQVPPVPSQDILLVEH 235
 DB 181 AQPPLLLLLLPLVGLLLAAACLMHQMORTRRTPRPGQVPPVPSQDILLVEH 235

RESULT 6

AAR66175 standard; Peptide; 235 AA.

AAR66175;

10-AUG-1995 (first entry)

Human S86/S109 Flt3 ligand peptide sequence.

Flt3 ligand; tyrosine kinase receptor ligand.

Homo sapiens.

WO9426891-A.

24-NOV-1994.

18-MAY-1994; 94WO-US05150.

19-MAY-1993; 93US-0065231.

07-JUL-1993; 93US-0089263.

16-JUL-1993; 93US-0092549.

13-AUG-1993; 93US-0106340.

24-AUG-1993; 93US-0112391.

19-NOV-1993; 93US-0155111.

03-DEC-1993; 93US-0162413.

(INRM) INST NAT SANTE & RECH MEDICALE.

(SCHE) SCHERING CORP.

Blindbaum D, Culpepper JA, Hannum CH, Lee FD;

WPI; 1995-006787/01.

N-PSDB; AA079642.

New ligand for the Flt3 tyrosine kinase receptor - and related
 nucleic acid, vectors, host cells and antibodies, useful for
 treating abnormal cell physiology and proliferation, e.g. cancer,
 also for diagnosis and drug screening

Claim 11; Page 76-77; 90pp; English.

A cDNA library from the human stromal cell line 28Sv48, in
 pME18S, was screened with an 800 bp fragment derived from
 mouse clone T110. This fragment encompasses the coding region
 conserved between two mouse clones, T118 and T110. Approx. 20
 positive clones were selected and partially sequenced. Two
 clones, S86 and S109, were found to be approx. 75% homologous
 to the mouse clones over the first 163 AAs. Clone S86 continued
 to show homology to T110 until the stop codon, although to a
 lesser degree, for an overall homology of 66%. Clones T118 and
 S109 do not show homology to each other or to the other clones
 after mouse residue 163 (human residue 160). An additional mouse
 clone designated M88 has a 29 AA insert at the junction between
 the common and divergent portions of the mouse ligand.

Sequence 235 AA:

Query Match 99.5%; Score 1236; DB 16; Length 235;
 Best Local Similarity 99.6%; Pred. No. 1.8e-108;
 Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
 DB 1 MTVLAPAMSPPTTYLLLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
 QY 61 ASNIQDEELCGALMRLVLAQRMERLKTVAAGSKMGLERVTETHEFTKCAFOPPSCL 120
 DB 61 ASNIQDEELCGALMRLVLAQRMERLKTVAAGSKMGLERVTETHEFTKCAFOPPSCL 120
 QY 121 REVQNTISRLQETSEQLVAKPWITRONFSRCLELOCOPDSSTLPVPSPPLEXTAPT 180
 DB 121 REVQNTISRLQETSEQLVAKPWITRONFSRCLELOCOPDSSTLPVPSPPLEXTAPT 180
 QY 181 APQPPULLLLLPVGLLLAAMCLHMORTRRTPRPGQVPPVPSPODLLLVEH 235
 DB 181 APQPPULLLLLPVGLLLAAMCLHMORTRRTPRPGQVPPVPSPODLLLVEH 235

RESULT 7
 AAB20194 standard; Protein; 235 AA.
 AC AAB20194;
 XX 14-MAY-2001 (first entry)
 DT Human Flt-3 ligand.
 DE Human Flt-3 ligand.
 KW Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;
 KM immunotherapy; therapy; tumour; cancer; melanoma; glioma;
 KW lymphoma; autoimmune disease; infection; gene therapy.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..26
 FT Protein /label= Signal_peptide
 FT /label= Mature_protein
 FT Domain 27..182
 FT /label= Extracellular_domain
 FT Domain 183..205
 FT /label= Transmembrane_domain
 FT Domain 206..235
 FT /label= Cytoplasmic_domain
 PN WO200109303-A2.
 PD 08-FEB-2001.
 XX
 XX 31-JUL-2000; 2000WO-US20679.
 XX
 XX 30-JUL-1999; 99US-0146170.
 XX (VICA-) VICAL INC.
 XX
 XX Hermanson GG;
 XX
 XX WPI: 2001-123319/13.
 XX N-PSDB; AAF30312.
 DR
 XX Immunogenic compositions comprising Flt-3 ligand encoding
 PT polynucleotide and one or more antigen, or cytokine encoding
 PT polynucleotide, useful for suppressing tumour growth and for treating
 PT autoimmune diseases (e.g. rheumatoid arthritis)
 XX
 XX Claim 2: Page 137-138; 149pp; English.
 XX
 XX The present sequence is that of human Fms-like tyrosine kinase
 CC (Flt-3 ligand). The invention is directed to enhancing the

CC Immune response of a vertebrate to an antigen or a cytokine by
 CC administering in vivo, into a tissue of a vertebrate, a Flt-3
 CC ligand-encoding polynucleotide, and 1 or more antigen- or
 CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding
 CC polynucleotide may encode the present full-length human Flt-3
 CC ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235
 CC of the Flt-3 ligand. The polynucleotides are incorporated into
 CC the cells of the vertebrate in vivo, and a prophylactically or
 CC therapeutically effective amount of Flt-3 ligand and 1 or more
 CC antigens or cytokines is produced in vivo. Pharmaceutical
 CC compositions comprising the polynucleotides are useful for
 CC suppressing tumour growth in a mammal. The tumour is melanoma,
 CC glioma or lymphoma, particularly B-cell lymphoma. They can also
 CC be used for the prophylactic and/or therapeutic treatment of:
 CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B
 CC and C in humans), parasitic (e.g. malaria) and fungal infections;
 CC (b) autoimmune diseases (e.g. rheumatoid arthritis and
 CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.
 CC Various other examples of these diseases are given in the
 CC specification.
 XX
 XX Sequence 235 AA:
 SQ

Query Match 99.5%; Score 1236; DB 22; Length 235;
 Best Local Similarity 99.6%; Pred. No. 1.8e-108;
 Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
 DB 1 MTVLAPAMSPPTTYLLLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60
 QY 61 ASNIQDEELCGALMRLVLAQRMERLKTVAAGSKMGLERVTETHEFTKCAFOPPSCL 120
 DB 61 ASNIQDEELCGALMRLVLAQRMERLKTVAAGSKMGLERVTETHEFTKCAFOPPSCL 120
 QY 121 REVQNTISRLQETSEQLVAKPWITRONFSRCLELOCOPDSSTLPVPSPPLEXTAPT 180
 DB 121 REVQNTISRLQETSEQLVAKPWITRONFSRCLELOCOPDSSTLPVPSPPLEXTAPT 180
 QY 181 APQPPULLLLLPVGLLLAAMCLHMORTRRTPRPGQVPPVPSPODLLLVEH 235
 DB 181 APQPPULLLLLPVGLLLAAMCLHMORTRRTPRPGQVPPVPSPODLLLVEH 235

RESULT 8
 AAY69721 standard; Protein; 212 AA.
 ID AAY69721
 XX AAY69721;
 XX
 XX 05-JUL-2000 (first entry)
 DT Human Flt-3 mutein L-3H.
 XX
 XX
 XX Immunomodulator; immunosuppressive; cytostatic; anti-anemic; anti-HIV;
 KW neuroprotective; antiallergic; Flt3 ligand; Flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hemopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutein.
 XX
 XX Homo sapiens.
 OS
 OS Synthetic.
 PN WO200001823-A2.
 XX
 XX 13-JAN-2000.
 PD
 XX 25-JUN-1999; 99WO-US14296.
 XX
 XX 02-JUL-1998; 98US-0109100.
 XX

PA (IMM) IMMUNEX CORP.
 XX
 PI Graddis TJ, McGrew JT;
 XX
 DR WPI: 2000-182115/16.
 XX
 PT Mutant soluble flt-3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions
 PT contains amino acid substitutions at positions 8, 84, 118 or 122
 XX
 PS Claim 4; Page 79-80; 90pp; English.

CC The invention relates to novel soluble flt-3 ligand (flt-3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AA69719) or mature (AA69720) flt-3-L
 CC polypeptides. This sequence represents an example of the novel flt-3
 CC ligand and comprises the L-3H mutant polypeptide. The flt-3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt-3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.

SO Sequence 212 AA:

Query Match 90.5%; Score 1124; DB 21; Length 212;
 Best Local Similarity 100.0%; Pred. No. 5.9e-98;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 SCQDPSFQHSPISSDFAVKIRLSYLLQDYVTVASNLQDEELCGGLMRLVLAQRMERL 84
 DB 2 SEQDPSFQHSPISSDFAVKIRLSYLLQDYVTVASNLQDEELCGGLMRLVLAQRMERL 61
 QY 85 RUKTVAGSKMOGLLEVRNTEIHFTVKCAFOPPSCLEFVQTNISRLQETSSEOLVALKPM 144
 DB 62 RUKTVAGSKMOGLLEVRNTEIHFTVKCAFOPPSCLEFVQTNISRLQETSSEOLVALKPM 121
 QY 145 ITRONSRCLELQCCPDSSSTLPPMSPRPLEATAPAPAPPLLLLLPVGLLLAAAC 204
 DB 122 ITRONSRCLELQCCPDSSSTLPPMSPRPLEATAPAPAPPLLLLLPVGLLLAAAC 181
 QY 205 LHMQRTRRTPRGEOVPPVPSPODLLVEH 235
 DB 182 LHMQRTRRTPRGEOVPPVPSPODLLVEH 212

RESULT 9

AA699007
 ID AA69007 standard; peptide; 209 AA.

AC AA69007;

XX 01-OCT-1998 (first entry)

DE Human flt-3 receptor agonist.

XX Human; flt-3 receptor agonist; haematopoietic cell stimulation; cancer;
 KW bone marrow reconstitution; haematological disease; immune deficiency;
 KW drug-induced myelosuppression; renal dialysis; gene therapy; infection;
 KM congenital metabolic disease; neurological disease; therapy;
 KM dendritic cell production.

XX Homo sapiens.

XX MO9818923-31.

XX

PD 07-MAY-1998.
 XX
 PF 23-OCT-1997; 97MO-US18700.
 XX
 PR 25-OCT-1996; 9605-0030094.
 XX
 PA (SEAR) SEARLE & CO G D.
 XX
 PI Feng Y, McEearn JP, McWhorter CA, Minnerly JC, Minster NT;
 PI Staten NR, Streeter PR, Woulfe SL;
 XX
 DR WPI: 1998-272218/24.
 XX
 PS Rearranged flt-3 receptor agonists and nucleic acids encoding them
 PT used to stimulate production of haematopoietic and dendritic cells,
 PT for treatment of haematological diseases, bone marrow reconstitution
 PT and in gene therapy

PS Disclosure; Page 9-10; 158pp; English.

CC This sequence represents a rearranged human flt-3 receptor agonists of
 CC the invention. The agonists have a modified flt-3 ligand amino acid
 CC sequence. The agonists are used to stimulate production of haematopoietic
 CC cells in vivo (e.g. in a subject about to donate blood) or for ex vivo
 CC expansion for subsequent transplantation, e.g. to reconstitute bone
 CC marrow after chemotherapy, disease etc., or to treat haematological
 CC disease such as drug-induced myelosuppression, defects caused by
 CC infections, burns or renal dialysis. Optionally ex vivo expanded cells
 CC are transduced with a gene therapy vector for treating e.g. congenital
 CC metabolic diseases, immune deficiency, neurological disease, cancer and
 CC infections. The agonists can also be used in the treatment of tumours,
 CC infections and autoimmune disease, when administered optionally with an
 CC antigen. The agonist can also be used in the production of dendritic
 CC cells for use as an immunising adjuvant for treatment disorders including
 CC acquired immune deficiency syndrome. Compared with native ligands, the
 CC new agonists have better stimulatory activity, reduced side effects
 CC and/or better physical properties such as solubility, stability or re-fold
 CC efficiency. When used together with other stimulatory agents, the
 CC agonists provide a synergistic effect.

SO Sequence 209 AA:

Query Match 89.7%; Score 1114; DB 19; Length 209;
 Best Local Similarity 100.0%; Pred. No. 5.1e-97;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRLSYLLQDYVTVASNLQDEELCGGLMRLVLAQRMERL 86
 DB 1 TODCSFQHSPISSDFAVKIRLSYLLQDYVTVASNLQDEELCGGLMRLVLAQRMERL 60
 QY 87 KTVAGSKMOGLLEVRNTEIHFTVKCAFOPPSCLEFVQTNISRLQETSSEOLVALKPMIT 146
 DB 61 KTVAGSKMOGLLEVRNTEIHFTVKCAFOPPSCLEFVQTNISRLQETSSEOLVALKPMIT 120
 QY 147 RQNFRCLELQCCPDSSSTLPPMSPRPLEATAPAPAPPLLLLLPVGLLLAAAC 206
 DB 121 RQNFRCLELQCCPDSSSTLPPMSPRPLEATAPAPAPPLLLLLPVGLLLAAAC 180
 QY 207 WQTRRTTRTPRGEOVPPVPSPODLLVEH 235
 DB 181 WQTRRTTRTPRGEOVPPVPSPODLLVEH 209

RESULT 10

AA69720
 ID AA69720 standard; Protein; 209 AA.

AC AA69720;

XX 05-JUL-2000 (first entry)

DE Mature wild type human flt-3 protein.

XX

KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia.
 XX
 OS Homo sapiens.
 PN WO200001823-A2.
 PD 13-JAN-2000.
 XX
 XX 25-JUN-1999; 99WO-US14296.
 XX
 XX 02-JUL-1998; 98US-0109100.
 XX
 XX (IMNV) IMMUNEX CORP.
 XX
 XX Graddis TJ, McGrew JT;
 DR WPI: 2000-182115/16.
 DR N-PSDB: AA259064.
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions,
 PT contains amino acid substitutions at positions 8, 84, 118 or 122
 XX
 PS Claim 1; Page 89-90; 90pp; English.
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AA169719) or mature (this sequence) flt3-L
 CC polypeptides. The flt3-L protein binds cell surface tyrosine kinase
 CC receptors and regulate growth and differentiation of hematopoietic
 CC progenitor cells. The flt3-L protein can be used to induce cellular
 CC expansion (especially in vivo) or differentiation, e.g. in
 CC hematopoietic, natural killer (NK) or dendritic cells, especially in the
 CC presence of growth factors such as interleukins, colony stimulating
 CC factors or protein kinases. The protein can also modulate, augment or
 CC enhance a patient's immune response and can be used to treat an immune
 CC disorder (e.g. allergy, autoimmunity or immunosuppression). The protein
 CC may be used to treat a pathological condition e.g. myelodysplasia,
 CC aplastic anemia, HIV infection, breast, small cell lung, testicular or
 CC ovarian cancer, lymphoma, multiple myeloma, neuroblastoma or acute
 CC leukemia.
 CC
 XX
 SO Sequence 209 AA;
 Query Match 89.7%; Score 1114; DB 21; Length 209;
 Best Local Similarity 100.0%; Pred. No. 5.1e-97;
 Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 TOPCSFOHSPSSDPFAVKIRELSYLLDDYPTVVASNLQDEELCGGLMRLVLAQRMRERL 86
 Db 1 TOPCSFOHSPSSDPFAVKIRELSYLLDDYPTVVASNLQDEELCGGLMRLVLAQRMRERL 60
 QY 87 KTVAGSKMOGLLELVNTEIHFTVKCAFOPPPSCIRFVQTNISRLQETSQOLVALKPMWT 146
 Db 61 KTVAGSKMOGLLELVNTEIHFTVKCAFOPPPSCIRFVQTNISRLQETSQOLVALKPMWT 120
 QY 147 RQNSRCLLELOCOPDSSSTLPPWSPRPLEATAFTAPQPLLLLLLPVGLLLAAAMCCH 206
 Db 121 RQNSRCLLELOCOPDSSSTLPPWSPRPLEATAFTAPQPLLLLLLPVGLLLAAAMCCH 180
 QY 207 WQRRRRTPRGEQVPPVSPQDILLVEH 235
 Db 181 WQRRRRTPRGEQVPPVSPQDILLVEH 209
 RESULT 11
 AAY69723

ID AAY69723 standard; Protein; 209 AA.
 XX
 XX AAY69723;
 AC
 XX
 DT 05-JUL-2000 (first entry)
 XX
 XX
 DE Human flt-3 mutein K84E.
 XX
 KW Immunomodulator; immunosuppressive; cytostatic; antianemic; anti-HIV;
 KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 KW cellular expansion; cellular differentiation; natural killer cell;
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 KW multiple myeloma; leukemia; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN WO200001823-A2.
 PD 13-JAN-2000.
 XX
 XX 25-JUN-1999; 99WO-US14296.
 XX
 XX 02-JUL-1998; 98US-0109100.
 XX
 XX (IMNV) IMMUNEX CORP.
 XX
 XX Graddis TJ, McGrew JT;
 DR WPI: 2000-182115/16.
 DR
 XX
 PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 PT immune response stimulation or treatment of pathological conditions,
 PT contains amino acid substitutions at positions 8, 84, 118 or 122
 XX
 PS Claim 4; Page 84-85; 90pp; English.
 CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AA169719) or mature (AAY69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt3-L
 CC ligands and comprises the K84E mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.
 CC
 XX
 SO Sequence 209 AA;
 Query Match 89.4%; Score 1110; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 1.2e-96;
 Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 27 TOPCSFOHSPSSDPFAVKIRELSYLLDDYPTVVASNLQDEELCGGLMRLVLAQRMRERL 86
 Db 1 TOPCSFOHSPSSDPFAVKIRELSYLLDDYPTVVASNLQDEELCGGLMRLVLAQRMRERL 60
 QY 87 KTVAGSKMOGLLELVNTEIHFTVKCAFOPPPSCIRFVQTNISRLQETSQOLVALKPMWT 146
 Db 61 KTVAGSKMOGLLELVNTEIHFTVKCAFOPPPSCIRFVQTNISRLQETSQOLVALKPMWT 120
 QY 147 RQNSRCLLELOCOPDSSSTLPPWSPRPLEATAFTAPQPLLLLLLPVGLLLAAAMCCH 206
 Db 147 RQNSRCLLELOCOPDSSSTLPPWSPRPLEATAFTAPQPLLLLLLPVGLLLAAAMCCH 206

CC myeloma, neuroblastoma or acute leukemia.
 XX Sequence 209 AA:
 SQ Query Match 89.4%; Score 1110; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 1.2e-96;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTASNLQDEELCGGLMRLVLAQRMERL 86
 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTASNLQDEELCGGLMRLVLAQRMERL 60

DB 87 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 146
 61 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 120

OY 147 RQNFSCLELQCCPDSSSTLPPWSPRPLEATAPAPQPELLLLLPVGLLLAAACMLH 206
 121 RQNFSCLELQCCPDSSSTLPPWSPRPLEATAPAPQPELLLLLPVGLLLAAACMLH 180

DB 207 WQTRRRTPRGEQVPVPSPDILLVEH 235
 181 WQTRRRTPRGEQVPVPSPDILLVEH 209

RESULT 14
 AAY69729
 ID AAY69729 standard; Protein: 209 AA.
 AC AAY69729;
 DT 05-JUL-2000 (first entry)
 DE Human flt-3 mutain A64T.

XX Immunomodulator; immunosuppressive; cytostatic; anti-anemic; anti-HIV;
 XX neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 XX cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 XX cellular expansion; cellular differentiation; natural killer cell;
 XX cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 XX myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 XX multiple myeloma; leukemia; mutain.

OS Homo sapiens.
 OS Synthetic.
 PN WO200001823-A2.
 XX 13-JAN-2000.
 PD 25-JUN-1999; 99MO-US14296.
 PF 02-JUL-1998; 98US-0109100.
 PR (IMMV) IMMUNEX CORP.
 PA Graddis TJ, McGrew JT;
 PI WPI: 2000-182115/16.
 DR Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 XX immune response stimulation or treatment of pathological conditions,
 XX contains amino acid substitutions at positions 8, 84, 118 or 122
 XX Claim 13; Page 78-79; 90pp; English.

CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AAY69719) or mature (AAY69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt3
 CC ligands and comprises the L26F mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can

CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins.
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.

XX Sequence 209 AA:
 SQ Query Match 89.4%; Score 1110; DB 21; Length 209;
 Best Local Similarity 99.5%; Pred. No. 1.2e-96;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

27 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTASNLQDEELCGGLMRLVLAQRMERL 86
 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPVTASNLQDEELCGGLMRLVLAQRMERL 60

DB 87 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 146
 61 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 120

OY 147 RQNFSCLELQCCPDSSSTLPPWSPRPLEATAPAPQPELLLLLPVGLLLAAACMLH 206
 121 RQNFSCLELQCCPDSSSTLPPWSPRPLEATAPAPQPELLLLLPVGLLLAAACMLH 180

DB 207 WQTRRRTPRGEQVPVPSPDILLVEH 235
 181 WQTRRRTPRGEQVPVPSPDILLVEH 209

RESULT 15
 AAY69722
 ID AAY69722 standard; Protein: 209 AA.
 AC AAY69722;
 DT 05-JUL-2000 (first entry)
 DE Human flt-3 mutain H8Y.

XX Immunomodulator; immunosuppressive; cytostatic; anti-anemic; anti-HIV;
 XX neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;
 XX cell surface tyrosine kinase receptor; hematopoietic progenitor cell;
 XX cellular expansion; cellular differentiation; natural killer cell;
 XX cancer; dendritic cell; immune response; autoimmunity; immunosuppression;
 XX myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;
 XX multiple myeloma; leukemia; mutain.

OS Homo sapiens.
 OS Synthetic.
 PN WO200001823-A2.
 XX 13-JAN-2000.
 PD 25-JUN-1999; 99MO-US14296.
 PF 02-JUL-1998; 98US-0109100.
 PR (IMMV) IMMUNEX CORP.
 PA Graddis TJ, McGrew JT;
 PI WPI: 2000-182115/16.
 DR Mutant soluble flt3 ligand polypeptide used in cellular expansion,
 XX immune response stimulation or treatment of pathological conditions,
 XX contains amino acid substitutions at positions 8, 84, 118 or 122
 XX Claim 13; Page 78-79; 90pp; English.

PS Claim 4; Page 81-82; 90pp; English.

XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides
 CC which exhibits increased or decreased biological activity relative to
 CC the full length wild type (AA69719) or mature (AA69720) flt3-L
 CC polypeptides. This sequence represents an example of the novel flt-3
 CC ligands and comprises the H87 mutant polypeptide. The flt3-L protein
 CC binds cell surface tyrosine kinase receptors and regulate growth and
 CC differentiation of hematopoietic progenitor cells. The flt3-L protein can
 CC be used to induce cellular expansion (especially in vivo) or
 CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic
 CC cells, especially in the presence of growth factors such as interleukins,
 CC colony stimulating factors or protein kinases. The protein can also
 CC modulate, augment or enhance a patient's immune response and can be used
 CC to treat an immune disorder (e.g. allergy, autoimmunity or
 CC immunosuppression). The protein may be used to treat a pathological
 CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,
 CC small cell lung, testicular or ovarian cancer, lymphoma, multiple
 CC myeloma, neuroblastoma or acute leukemia.

SO Sequence 209 AA;

Query Match 89.2%; Score 1108; DB 21; Length 209;

Best Local Similarity 99.5%; Pred. No. 1,9e-96;

Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TDCCSFQHSPISSDFAVKIRELSDYLLQDIPYVVASNLQDEELCGGLMRLVLAQRMERL 86
 DB 1 TDCCSFQHSPISSDFAVKIRELSDYLLQDIPYVVASNLQDEELCGGLMRLVLAQRMERL 60
 QY 87 KTVAGSKMGLERVTETHEFTKCAFOPPSSGLRFYQTNISRLQETSQVLAQKRWIT 146
 DB 61 KTVAGSKMGLERVTETHEFTKCAFOPPSSGLRFYQTNISRLQETSQVLAQKRWIT 120
 QY 147 RQNFSTRCLQCCPDSSSTLPMPSPRLPENTAPAPPLLLLLFPVGLLLAAACLN 206
 DB 121 RQNFSTRCLQCCPDSSSTLPMPSPRLPENTAPAPPLLLLLFPVGLLLAAACLN 180
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 DB 181 MORTRRRTPRPGQVPPVSPDILLVEH 209

Search completed: May 27, 2003, 18:27:13

Job time : 37 secs

GenCore version 5.1.4-p5-4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2003, 18:28:06 ; Search time 57 Seconds
(Without alignments)
408.870 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242
Sequence: 1 MTYLAPAWSPRTYLLILL.....RPGQVPPSPQDLLVER 235

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 375593 seqs, 9917265 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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11: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1242	100.0	235	9	US-10-095-449-6
2	1242	100.0	235	10	US-09-448-378-1
3	1242	100.0	235	10	US-09-983-806-6
4	1242	100.0	235	10	US-09-904-536-1
5	1124	90.5	212	10	US-08-904-536-10
6	1114	89.7	209	10	US-08-904-536-18
7	1110	89.4	209	10	US-09-904-536-9
8	1110	89.4	209	10	US-09-904-536-12
9	1110	89.4	209	10	US-09-904-536-14
10	1110	89.4	209	10	US-09-904-536-17
11	1108	89.2	209	10	US-09-904-536-11
12	1108	89.2	209	10	US-09-904-536-15
13	1107	89.1	209	10	US-09-904-536-13
14	1106	89.0	209	10	US-09-904-536-8
15	1100	88.6	209	10	US-09-904-536-16
16	822	66.2	156	9	US-10-053-355A-1
17	768.5	61.9	231	9	US-10-095-449-2
18	768.5	61.9	231	10	US-09-448-378-2
19	768.5	61.9	231	10	US-09-983-806-2

20	506.5	40.8	137	10	US-09-904-536-19	Sequence 19, Appl
21	91.5	7.4	674	10	US-09-899-471-2	Sequence 2, Appl
22	91.5	7.4	698	9	US-09-866-050A-509	Sequence 509, App
23	91.5	7.4	698	9	US-09-863-818A-8	Sequence 8, Appl
24	89.5	7.4	698	10	US-09-899-471-5	Sequence 5, Appl
25	89.5	7.2	874	10	US-09-826-508-26	Sequence 26, Appl
26	89.5	7.2	941	9	US-09-793-139-47	Sequence 47, Appl
27	89.5	7.2	941	9	US-10-300-616-31	Sequence 31, Appl
28	89.5	7.2	941	10	US-09-818-879-47	Sequence 47, Appl
29	89.5	7.2	941	10	US-09-211-755B-47	Sequence 47, Appl
30	88.5	7.1	1257	9	US-10-109-324-2	Sequence 2, Appl
31	88	7.1	238	9	US-10-174-363-30	Sequence 30, Appl
32	87.5	7.0	415	9	US-09-917-372-20	Sequence 20, Appl
33	87.5	7.0	415	10	US-09-826-212-6	Sequence 6, Appl
34	87.5	7.0	415	10	US-09-907-372-20	Sequence 20, Appl
35	87.5	7.0	415	10	US-09-935-727-8	Sequence 8, Appl
36	87.5	7.0	479	9	US-10-108-605-57	Sequence 57, Appl
37	87.5	7.0	570	9	US-09-991-496-104	Sequence 104, App
38	87.5	7.0	570	10	US-09-874-923-104	Sequence 104, App
39	85.5	6.9	519	10	US-09-925-300-1680	Sequence 1680, Ap
40	84.5	6.8	610	10	US-09-783-708-1	Sequence 1, Appl
41	84.5	6.8	913	10	US-09-223-490-4	Sequence 4, Appl
42	84.5	6.8	1134	9	US-10-001-873-50	Sequence 50, Appl
43	84	6.8	107	10	US-09-220-920-52	Sequence 52, Appl
44	84	6.8	220	9	US-10-001-054-56	Sequence 56, Appl
45	84	6.8	220	10	US-09-220-920-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-10-095-449-6
Sequence 6, Application US/10095449
Patent No. US20020160004A1

GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,449
FILING DATE: 13-Mar-2002
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/669,692
FILING DATE: 24-JUN-1996
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644
 TELE: 756822
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 235 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-10-095-449-6

Query Match 100.0%; Score 1242; DB 9; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1,4e-101;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTLPAMSTPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
 DB 1 MVTLPAMSTPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
 QY 61 ASNLQDEELCGGLMRVLAQRMERLKTVAAGSKMGLLEVNTEIHFVTKCAFQPPSCL 120
 DB 61 ASNLQDEELCGGLMRVLAQRMERLKTVAAGSKMGLLEVNTEIHFVTKCAFQPPSCL 120
 QY 121 REVQTNISRLQETSEQLVAKPWITRONFSRCLQOCOPDSSSTLPMPSPRPLEATAPT 180
 DB 121 REVQTNISRLQETSEQLVAKPWITRONFSRCLQOCOPDSSSTLPMPSPRPLEATAPT 180
 QY 181 APOPLLILLPVGLLLAAACLHMORTRRRTPRPGEQVPVPSPQDLLLVEH 235
 DB 181 APOPLLILLPVGLLLAAACLHMORTRRRTPRPGEQVPVPSPQDLLLVEH 235

RESULT 2
 US-09-448-378-1

; Sequence 1, Application US/09448378
 ; Patent No. US20020034517A1
 GENERAL INFORMATION:
 APPLICANT: Brasel, Kenneth
 TITLE OF INVENTION: Dendritic Cell Stimulatory Factor
 FILE REFERENCE: 2836-D
 CURRENT APPLICATION NUMBER: US/09/448,378
 CURRENT FILING DATE: 1999-11-23
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 1
 LENGTH: 235
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-448-378-1

Query Match 100.0%; Score 1242; DB 10; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1,4e-101;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTLPAMSTPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
 DB 1 MVTLPAMSTPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
 QY 61 ASNLQDEELCGGLMRVLAQRMERLKTVAAGSKMGLLEVNTEIHFVTKCAFQPPSCL 120
 DB 61 ASNLQDEELCGGLMRVLAQRMERLKTVAAGSKMGLLEVNTEIHFVTKCAFQPPSCL 120
 QY 121 REVQTNISRLQETSEQLVAKPWITRONFSRCLQOCOPDSSSTLPMPSPRPLEATAPT 180
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 QY 181 APOPLLILLPVGLLLAAACLHMORTRRRTPRPGEQVPVPSPQDLLLVEH 235
 DB 181 APOPLLILLPVGLLLAAACLHMORTRRRTPRPGEQVPVPSPQDLLLVEH 235

RESULT 3
 US-09-983-806-6

; Sequence 6, Application US/09983806
 ; Patent No. US20020107365A1
 GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
 TITLE OF INVENTION: Ligands for f13/f1k-2 Receptors
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: Washington
 COUNTRY: US
 ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.0.1
 SOFTWARE: Microsoft Word, Version #5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/983,806
 FILING DATE: 25-Oct-2001
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/444,626
 FILING DATE: 19-MAY-1995
 APPLICATION NUMBER: US 08/162,407
 FILING DATE: 03-DEC-1993
 APPLICATION NUMBER: 08/111,758
 FILING DATE: August 25, 1993
 APPLICATION NUMBER: 08/106,463
 FILING DATE: August 12, 1993
 APPLICATION NUMBER: 08/068,394
 FILING DATE: May 24, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Malaska, Stephen L.
 REGISTRATION NUMBER: 32,655
 REFERENCE/DOCKET NUMBER: 2813-C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0644
 TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
 LENGTH: 235 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-983-806-6

Query Match 100.0%; Score 1242; DB 10; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1,4e-101;
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MVTLPAMSTPTTYLLLLSSGLSGTDCSFQHSPISSDFAVKIRELSYLLQDYPTV 60
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 DB 61 ASNLQDEELCGGLMRVLAQRMERLKTVAAGSKMGLLEVNTEIHFVTKCAFQPPSCL 120
 QY 121 REVQTNISRLQETSEQLVAKPWITRONFSRCLQOCOPDSSSTLPMPSPRPLEATAPT 180
 DB 121 REVQTNISRLQETSEQLVAKPWITRONFSRCLQOCOPDSSSTLPMPSPRPLEATAPT 180
 QY 181 APOPLLILLPVGLLLAAACLHMORTRRRTPRPGEQVPVPSPQDLLLVEH 235
 DB 181 APOPLLILLPVGLLLAAACLHMORTRRRTPRPGEQVPVPSPQDLLLVEH 235

RESULT 4

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US-09-904-536-1
: Sequence 1, Application US/09904536
: Patent No. US20020111475A1
: GENERAL INFORMATION:
: APPLICANT: Graddis, Thomas J.
: APPLICANT: McGrew, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03260.0028
: CURRENT APPLICATION NUMBER: US/09/904,536
: CURRENT FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
: PRIOR FILING DATE: 1999-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 1
: LENGTH: 235
: TYPE: PRF
: ORGANISM: Homo sapiens
US-09-904-536-1

Query Match          100.0%; Score 1242; DB 10; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.4e-101;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 RFVQTNISRLLOETSEQLVAKLPATTRONFSRCLQCCPDSSSTLPMPSPRPLEATAP 180
QY 181 APOPLLPLLLPVGLLLAAACLMQTRRRTPRPGQVPPVSPDOLLVEH 235
DB 181 APOPLLPLLLPVGLLLAAACLMQTRRRTPRPGQVPPVSPDOLLVEH 235

RESULT 5
US-09-904-536-10
: Sequence 10, Application US/09904536
: Patent No. US20020111475A1
: GENERAL INFORMATION:
: APPLICANT: Graddis, Thomas J.
: APPLICANT: McGrew, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03260.0028
: CURRENT APPLICATION NUMBER: US/09/904,536
: CURRENT FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
: PRIOR FILING DATE: 1999-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 10
: LENGTH: 212
: TYPE: PRF
: ORGANISM: Homo sapiens
US-09-904-536-10

Query Match          90.5%; Score 1124; DB 10; Length 212;
Best Local Similarity 100.0%; Pred. No. 3e-91;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 SGTODCSFQHSPISSDFAVKIRELSDYLLQDYPVTYASNLQDEELCGMLRVLVAQRME 84
DB 2 SGTODCSFQHSPISSDFAVKIRELSDYLLQDYPVTYASNLQDEELCGMLRVLVAQRME 84
QY 85 RLKTVAGSKMOGLLERVTEIHFTVKCAFPQPPSCLRFVQTNISRLLOETSEQLVAKLP 144
DB 62 RLKTVAGSKMOGLLERVTEIHFTVKCAFPQPPSCLRFVQTNISRLLOETSEQLVAKLP 121
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QY 145 ITRQNFSCLELQCCPDSSSTLPMPSPRPLEATAPAPQPLLPLLLPVGLLLAAAC 204
DB 122 ITRQNFSCLELQCCPDSSSTLPMPSPRPLEATAPAPQPLLPLLLPVGLLLAAAC 181
QY 205 LHMQRTRRRTPRPGQVPPVSPDOLLVEH 235
DB 182 LHMQRTRRRTPRPGQVPPVSPDOLLVEH 212

RESULT 6
US-09-904-536-18
: Sequence 18, Application US/09904536
: Patent No. US20020111475A1
: GENERAL INFORMATION:
: APPLICANT: Graddis, Thomas J.
: APPLICANT: McGrew, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03260.0028
: CURRENT APPLICATION NUMBER: US/09/904,536
: CURRENT FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
: PRIOR FILING DATE: 1999-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 18
: LENGTH: 209
: TYPE: PRF
: ORGANISM: Homo sapiens
US-09-904-536-18

Query Match          89.7%; Score 1114; DB 10; Length 209;
Best Local Similarity 100.0%; Pred. No. 2.2e-90;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTYASNLQDEELCGMLRVLVAQRMERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTYASNLQDEELCGMLRVLVAQRMERL 60
QY 87 KTVAGSKMOGLLERVTEIHFTVKCAFPQPPSCLRFVQTNISRLLOETSEQLVAKLPIT 146
DB 61 KTVAGSKMOGLLERVTEIHFTVKCAFPQPPSCLRFVQTNISRLLOETSEQLVAKLPIT 120
QY 147 RQNFSCLELQCCPDSSSTLPMPSPRPLEATAPAPQPLLPLLLPVGLLLAAAC 206
DB 121 RQNFSCLELQCCPDSSSTLPMPSPRPLEATAPAPQPLLPLLLPVGLLLAAAC 180
QY 207 WQTRRRTPRPGQVPPVSPDOLLVEH 235
DB 181 WQTRRRTPRPGQVPPVSPDOLLVEH 209

RESULT 7
US-09-904-536-9
: Sequence 9, Application US/09904536
: Patent No. US20020111475A1
: GENERAL INFORMATION:
: APPLICANT: Graddis, Thomas J.
: APPLICANT: McGrew, Jeffrey T.
: TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
: FILE REFERENCE: 03260.0028
: CURRENT APPLICATION NUMBER: US/09/904,536
: CURRENT FILING DATE: 2001-07-16
: PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
: PRIOR FILING DATE: 1999-07-02
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 9
: LENGTH: 209
: TYPE: PRF
: ORGANISM: Homo sapiens
US-09-904-536-9
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Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 5e-90;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVANSNLODEELCGGLMRVLAQRMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVANSNLODEELCGGLMRVLAQRMERL 60
QY 87 KTVAGSKMOGLLEVRNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 146
DB 61 KTVAGSKMOGLLEVRNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 120
QY 147 RQNFSCLELOCQOPDSSSTLPMPSPRPLEATAPTAPOPLLILLPVGLLLAAACMH 206
DB 121 RQNFSCLELOCQOPDSSSTLPMPSPRPLEATAPTAPOPLLILLPVGLLLAAACMH 180
QY 207 WQTRRRTPRPGEOVPVPVSPDOLLVEH 235
DB 181 WQTRRRTPRPGEOVPVPVSPDOLLVEH 209

RESULT 8
US-09-904-536-12
; Sequence 12, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-12

Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 5e-90;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVANSNLODEELCGGLMRVLAQRMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVANSNLODEELCGGLMRVLAQRMERL 60
QY 87 KTVAGSKMOGLLEVRNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 146
DB 61 KTVAGSKMOGLLEVRNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 120
QY 147 RQNFSCLELOCQOPDSSSTLPMPSPRPLEATAPTAPOPLLILLPVGLLLAAACMH 206
DB 121 RQNFSCLELOCQOPDSSSTLPMPSPRPLEATAPTAPOPLLILLPVGLLLAAACMH 180
QY 207 WQTRRRTPRPGEOVPVPVSPDOLLVEH 235
DB 181 WQTRRRTPRPGEOVPVPVSPDOLLVEH 209

RESULT 9
US-09-904-536-14
; Sequence 14, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
```

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; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-14

Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 5e-90;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVANSNLODEELCGGLMRVLAQRMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVANSNLODEELCGGLMRVLAQRMERL 60
QY 87 KTVAGSKMOGLLEVRNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 146
DB 61 KTVAGSKMOGLLEVRNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 120
QY 147 RQNFSCLELOCQOPDSSSTLPMPSPRPLEATAPTAPOPLLILLPVGLLLAAACMH 206
DB 121 RQNFSCLELOCQOPDSSSTLPMPSPRPLEATAPTAPOPLLILLPVGLLLAAACMH 180
QY 207 WQTRRRTPRPGEOVPVPVSPDOLLVEH 235
DB 181 WQTRRRTPRPGEOVPVPVSPDOLLVEH 209

RESULT 10
US-09-904-536-17
; Sequence 17, Application US/09904536
; Patent No. US2002011475A1
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/904,536
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-536-17

Query Match      89.4%; Score 1110; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 5e-90;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVANSNLODEELCGGLMRVLAQRMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPTVANSNLODEELCGGLMRVLAQRMERL 60
QY 87 KTVAGSKMOGLLEVRNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 146
DB 61 KTVAGSKMOGLLEVRNTEIHFVTKCAFQPPSCLEFVQTNISRLQETSEQVALKPWIT 120
QY 147 RQNFSCLELOCQOPDSSSTLPMPSPRPLEATAPTAPOPLLILLPVGLLLAAACMH 206
DB 121 RQNFSCLELOCQOPDSSSTLPMPSPRPLEATAPTAPOPLLILLPVGLLLAAACMH 180
QY 207 WQTRRRTPRPGEOVPVPVSPDOLLVEH 235
DB 181 WQTRRRTPRPGEOVPVPVSPDOLLVEH 209
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US-09-904-536-8

Query Match 89.0%; Score 1106; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.1e-89;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLDYLDYPTVASNLODEELCGGLMRVLVAORMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLDYLDYPTVASNLODEELCGGLMRVLVAORMERL 60
QY 87 KTVAGSKMOGLERVTETHEFTKCAFOPPPSCLRFVQTNISRLQETSEQLVALKPMIT 146
DB 61 KTVAGSKMOGLERVTETHEFTKCAFOPPPSCLRFVQTNISRLQETSEQLVALKPMIT 120
QY 147 RQNFSCLELOCOPDSSSTLPWPSPRPLEATAPAPOPULLLLLPVGLLLAAACMH 206
DB 121 RQNFSCLELOCOPDSSSTLPWPSPRPLEATAPAPOPULLLLLPVGLLLAAACMH 180
QY 207 WQTRRRRTPRGQVPPVPSQDILLVEH 235
DB 181 WQTRRRRTPRGQVPPVPSQDILLVEH 209

RESULT 15

US-09-904-536-16
Sequence 16, Application US/09904536
Patent No. US2002011475A1
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-536-16

Query Match 88.6%; Score 1100; DB 10; Length 209;
Best Local Similarity 99.5%; Pred. No. 3.8e-89;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLDYLDYPTVASNLODEELCGGLMRVLVAORMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLDYLDYPTVASNLODEELCGGLMRVLVAORMERL 60
QY 87 KTVAGSKMOGLERVTETHEFTKCAFOPPPSCLRFVQTNISRLQETSEQLVALKPMIT 146
DB 61 KTVAGSKMOGLERVTETHEFTKCAFOPPPSCLRFVQTNISRLQETSEQLVALKPMIT 120
QY 147 RQNFSCLELOCOPDSSSTLPWPSPRPLEATAPAPOPULLLLLPVGLLLAAACMH 206
DB 121 RQNFSCLELOCOPDSSSTLPWPSPRPLEATAPAPOPULLLLLPVGLLLAAACMH 180
QY 207 WQTRRRRTPRGQVPPVPSQDILLVEH 235
DB 181 WQTRRRRTPRGQVPPVPSQDILLVEH 209

Search completed: May 27, 2003, 18:36:27
Job time : 58 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 27, 2003, 18:26:36 ; Search time 15 Seconds

(without alignments)
460.959 Million cell updates/sec

Title: US-08-994-468-6

Perfect score: 1242
Sequence: 1 MTVALPAPMSPTTILLILL...RPGQVPPVPSQDILLVHR 235

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents-AA:*
1: /cgn2-6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2-6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2-6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2-6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2-6/ptodata/1/1aa/PTUS.COMB.pep:*
6: /cgn2-6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1	US-08-243-545-6 Sequence 6, Appl
2	1242	100.0	235	2	US-08-993-962-6 Sequence 6, Appl
3	1242	100.0	235	4	US-09-160-841-6 Sequence 6, Appl
4	1242	100.0	235	4	US-09-109-100-1 Sequence 1, Appl
5	1242	100.0	235	5	PCT-US94-05365-6 Sequence 6, Appl
6	1124	90.5	212	4	US-09-109-100-10 Sequence 10, Appl
7	1114	89.7	209	4	US-09-109-100-18 Sequence 18, Appl
8	1110	89.4	209	4	US-09-109-100-9 Sequence 9, Appl
9	1110	89.4	209	4	US-09-109-100-12 Sequence 12, Appl
10	1110	89.4	209	4	US-09-109-100-14 Sequence 14, Appl
11	1110	89.4	209	4	US-09-109-100-17 Sequence 17, Appl
12	1108	89.2	209	4	US-09-109-100-11 Sequence 11, Appl
13	1108	89.2	209	4	US-09-109-100-15 Sequence 15, Appl
14	1107	89.1	209	4	US-09-109-100-13 Sequence 13, Appl
15	1106	89.0	209	4	US-09-109-100-8 Sequence 8, Appl
16	1100	88.6	209	4	US-09-109-100-16 Sequence 16, Appl
17	768.5	61.9	231	1	US-08-243-545-2 Sequence 2, Appl
18	768.5	61.9	231	2	US-08-993-962-2 Sequence 2, Appl
19	768.5	61.9	231	4	US-09-160-841-2 Sequence 2, Appl
20	768.5	61.9	231	5	PCT-US94-05365-2 Sequence 2, Appl
21	765.5	61.6	231	1	US-08-220-3798-7 Sequence 7, Appl
22	765.5	61.6	231	5	PCT-US95-03866-6 Sequence 6, Appl
23	506.5	40.8	137	4	US-09-109-100-19 Sequence 19, Appl
24	154	12.4	42	5	PCT-US94-05150-17 Sequence 17, Appl
25	91.5	7.4	675	1	US-08-317-522A-9 Sequence 9, Appl
26	91.5	7.4	675	1	US-08-439-818A-9 Sequence 9, Appl
27	91.5	7.4	675	2	US-08-751-965-9 Sequence 9, Appl

28	91.5	7.4	675	2	US-08-738-975-9	Sequence 9, Appl
29	91.5	7.4	675	2	US-08-728-626-9	Sequence 9, Appl
30	91.5	7.4	675	3	US-08-808-599A-9	Sequence 9, Appl
31	87.5	7.0	415	4	US-09-006-353A-6	Sequence 6, Appl
32	87.5	7.0	415	4	US-09-573-986-6	Sequence 6, Appl
33	85	6.8	366	1	US-08-004-992-8	Sequence 8, Appl
34	84.5	6.8	913	1	US-08-445-640-4	Sequence 4, Appl
35	84.5	6.8	913	3	US-08-170-558-4	Sequence 4, Appl
36	84.5	6.8	913	3	US-08-447-314-4	Sequence 4, Appl
37	84.5	6.8	107	4	US-08-445-461-4	Sequence 4, Appl
38	84	6.8	107	4	US-09-220-528-52	Sequence 52, Appl
39	84	6.8	220	4	US-09-220-528-26	Sequence 26, Appl
40	83.5	6.7	429	1	US-07-964-589-2	Sequence 2, Appl
41	83.5	6.7	429	5	PCT-US93-02024-2	Sequence 2, Appl
42	83.5	6.7	671	3	US-09-121-321-16	Sequence 16, Appl
43	83.5	6.7	671	4	US-08-933-803A-16	Sequence 16, Appl
44	83	6.7	28	5	PCT-US94-05150-12	Sequence 12, Appl
45	83	6.7	758	1	US-07-756-250-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-243-545-6
Sequence 6, Application US/08243545
Patent No. 5554512
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
TITLE OF INVENTION: Ligands for fli3/Flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
City: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,545
FILING DATE: 11-May-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,407
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-243-545-6

Query Match 100.0%; Score 1242; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLAPAMSPPTTYLLLLSSGLSGTDCSFQHPISDPFAVKIRELSDYLLQDYPYV 60
DB 1 MVLAPAMSPPTTYLLLLSSGLSGTDCSFQHPISDPFAVKIRELSDYLLQDYPYV 60
QY 61 ASNODEELCGGLWRLVLAORMERLKTAVAGSKMGGLELVNTEIHFVTKCAFQPPSCL 120
DB 61 ASNODEELCGGLWRLVLAORMERLKTAVAGSKMGGLELVNTEIHFVTKCAFQPPSCL 120
QY 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPWPSPRLATAPT 180
DB 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPWPSPRLATAPT 180
QY 181 APOPELLLLLPVGLLLAAWCLHMORTRRRTPRPEQVPVPVSPDILLVEH 235
DB 181 APOPELLLLLPVGLLLAAWCLHMORTRRRTPRPEQVPVPVSPDILLVEH 235

RESULT 2
US-08-993-962-6
Sequence 6, Application US/08993962
Patent No. 5843423

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,962
FILING DATE: December 18, 1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-993-962-6

Query Match 100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLAPAMSPPTTYLLLLSSGLSGTDCSFQHPISDPFAVKIRELSDYLLQDYPYV 60
DB 1 MVLAPAMSPPTTYLLLLSSGLSGTDCSFQHPISDPFAVKIRELSDYLLQDYPYV 60
QY 61 ASNODEELCGGLWRLVLAORMERLKTAVAGSKMGGLELVNTEIHFVTKCAFQPPSCL 120
DB 61 ASNODEELCGGLWRLVLAORMERLKTAVAGSKMGGLELVNTEIHFVTKCAFQPPSCL 120
QY 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPWPSPRLATAPT 180
DB 121 RFVOTNISRLQETSEQLVALKPWITRONFSRCLQCPDSSSTLPWPSPRLATAPT 180
QY 181 APOPELLLLLPVGLLLAAWCLHMORTRRRTPRPEQVPVPVSPDILLVEH 235
DB 181 APOPELLLLLPVGLLLAAWCLHMORTRRRTPRPEQVPVPVSPDILLVEH 235

RESULT 3
US-09-160-841-6
Sequence 6, Application US/09160841
Patent No. 6190655

GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0.1
SOFTWARE: Microsoft Word, Version #5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,841
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/162,407
FILING DATE: December 3, 1993
APPLICATION NUMBER: 08/111,758
FILING DATE: August 25, 1993

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/106,463
FILING DATE: August 12, 1993
APPLICATION NUMBER: 08/068,394
FILING DATE: May 24, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2813-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-160-841-6

Query Match 100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTVLAPAMSPPTTYLLLLSSGSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTY 60
QY 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGLLERNVTEIHFTVTKCAFQPPSCL 120
DB 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGLLERNVTEIHFTVTKCAFQPPSCL 120
QY 121 RFVQTNISRLQETSQDLVAKPWITRONFSRCLELQCPDSSSTLPWPSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSQDLVAKPWITRONFSRCLELQCPDSSSTLPWPSPRPLEATAPT 180
QY 181 APOPLLILLPLVGLLLAAACLMQRTRRTPRGEQVPPVPSPODLLVHEH 235
DB 181 APOPLLILLPLVGLLLAAACLMQRTRRTPRGEQVPPVPSPODLLVHEH 235

RESULT 4
US-09-109-100-1
Sequence 1, Application US/09109100C
Patent No. 6291661

GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-1

Query Match 100.0%; Score 1242; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTY 60
DB 1 MTVLAPAMSPPTTYLLLLSSGSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTY 60
QY 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGLLERNVTEIHFTVTKCAFQPPSCL 120
DB 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGLLERNVTEIHFTVTKCAFQPPSCL 120
QY 121 RFVQTNISRLQETSQDLVAKPWITRONFSRCLELQCPDSSSTLPWPSPRPLEATAPT 180
DB 121 RFVQTNISRLQETSQDLVAKPWITRONFSRCLELQCPDSSSTLPWPSPRPLEATAPT 180
QY 181 APOPLLILLPLVGLLLAAACLMQRTRRTPRGEQVPPVPSPODLLVHEH 235
DB 181 APOPLLILLPLVGLLLAAACLMQRTRRTPRGEQVPPVPSPODLLVHEH 235

RESULT 5
PCT-US94-05365-6
Sequence 6, Application PC/TUS9405365
GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephen L. Malaska, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05365
FILING DATE: May 24, 1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: -to be assigned-

FILING DATE: May 11, 1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/162,407

FILING DATE: December 3, 1993

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/111,758

FILING DATE: August 25, 1993

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/106,463

FILING DATE: August 12, 1993

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/068,394

FILING DATE: May 24, 1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2813-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

TELEFAX: (206) 233-0644

TELEX: 756822

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-05365-6

Query Match 100.0%; Score 1242; DB 5; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.7e-117;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTTYLLLLSSGSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTY 60
DB 1 MTVLAPAMSPPTTYLLLLSSGSGTDCSFQHSPISSDFAVKIRELSDYLLQDYPVTY 60
QY 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGLLERNVTEIHFTVTKCAFQPPSCL 120
DB 61 ASNLQDEELCGGLMRVLVAQRMERLKTVAAGSKMGLLERNVTEIHFTVTKCAFQPPSCL 120
QY 121 RFVQTNISRLQETSQDLVAKPWITRONFSRCLELQCPDSSSTLPWPSPRPLEATAPT 180


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Query Match      89.4%; Score 1110; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 3e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPYVASNLODEELCGGLMRLVLAQRMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPYVASNLODEELCGGLMRLVLAQRMERL 60

QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 146
DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 120

QY 147 RQNFSCLELOCOPDSSSTLPSPSPRLPPLAATAPOPLLILLPVGLLLAAACMLH 206
DB 121 RQNFSCLELOCOPDSSSTLPSPSPRLPPLAATAPOPLLILLPVGLLLAAACMLH 180

QY 207 WQTRRRTRPRGEOVPPVPSPODLLVEH 235
DB 181 WQTRRRTRPRGEOVPPVPSPODLLVEH 209

RESULT 10
US-09-109-100-14
Sequence 14, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: McGrew, Thomas J.
APPLICANT: Graddis, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 14
LENGTH: 209
TYPE: PRF
ORGANISM: Homo sapiens
US-09-109-100-14

Query Match      89.4%; Score 1110; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 3e-104;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPYVASNLODEELCGGLMRLVLAQRMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPYVASNLODEELCGGLMRLVLAQRMERL 60

QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 146
DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 120

QY 147 RQNFSCLELOCOPDSSSTLPSPSPRLPPLAATAPOPLLILLPVGLLLAAACMLH 206
DB 121 RQNFSCLELOCOPDSSSTLPSPSPRLPPLAATAPOPLLILLPVGLLLAAACMLH 180

QY 207 WQTRRRTRPRGEOVPPVPSPODLLVEH 235
DB 181 WQTRRRTRPRGEOVPPVPSPODLLVEH 209

RESULT 11
US-09-109-100-17
Sequence 17, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: McGrew, Thomas J.
APPLICANT: Graddis, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
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NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 17
LENGTH: 209
TYPE: PRF
ORGANISM: Homo sapiens
US-09-109-100-17

Query Match      89.4%; Score 1110; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 3e-104;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPYVASNLODEELCGGLMRLVLAQRMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPYVASNLODEELCGGLMRLVLAQRMERL 60

QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 146
DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 120

QY 147 RQNFSCLELOCOPDSSSTLPSPSPRLPPLAATAPOPLLILLPVGLLLAAACMLH 206
DB 121 RQNFSCLELOCOPDSSSTLPSPSPRLPPLAATAPOPLLILLPVGLLLAAACMLH 180

QY 207 WQTRRRTRPRGEOVPPVPSPODLLVEH 235
DB 181 WQTRRRTRPRGEOVPPVPSPODLLVEH 209

RESULT 12
US-09-109-100-11
Sequence 11, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: McGrew, Thomas J.
APPLICANT: Graddis, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 11
LENGTH: 209
TYPE: PRF
ORGANISM: Homo sapiens
US-09-109-100-11
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Query Match      89.2%; Score 1108; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 4.8e-104;
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 27 TODCSFQHSPISSDFAVKIRELSYLLQDYPYVASNLODEELCGGLMRLVLAQRMERL 86
DB 1 TODCSFQHSPISSDFAVKIRELSYLLQDYPYVASNLODEELCGGLMRLVLAQRMERL 60

QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 146
DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFOPPPSCLRFVOTNISRLLOETSEQVALKPMIT 120

QY 147 RQNFSCLELOCOPDSSSTLPSPSPRLPPLAATAPOPLLILLPVGLLLAAACMLH 206
DB 121 RQNFSCLELOCOPDSSSTLPSPSPRLPPLAATAPOPLLILLPVGLLLAAACMLH 180

QY 207 WQTRRRTRPRGEOVPPVPSPODLLVEH 235
DB 181 WQTRRRTRPRGEOVPPVPSPODLLVEH 209

RESULT 13
US-09-109-100-15
Sequence 15, Application US/09109100C
Patent No. 6291661
```

GENERAL INFORMATION:

APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-15

Query Match 89.2%; Score 1108; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 4,6e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLDYPYTVASNLQDEELCGGLMRVLVAQRMERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSYLLDYPYTVASNLQDEELCGGLMRVLVAQRMERL 60
QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146
DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120
QY 147 RQNFRCLELQCPDPSSTLPWPSPRPLEATAPAPQPLLLLLLPGVGLLLAAACLH 206
DB 121 RQNFRCLELQCPDPSSTLPWPSPRPLEATAPAPQPLLLLLLPGVGLLLAAACLH 180
QY 207 WQTRRRTPRPGQVPPVPSPODLLVEH 235
DB 181 WQTRRRTPRPGQVPPVPSPODLLVEH 209

RESULT 14

US-09-109-100-13
Sequence 13, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-13

Query Match 89.1%; Score 1107; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 6e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLDYPYTVASNLQDEELCGGLMRVLVAQRMERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSYLLDYPYTVASNLQDEELCGGLMRVLVAQRMERL 60
QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146
DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120
QY 147 RQNFRCLELQCPDPSSTLPWPSPRPLEATAPAPQPLLLLLLPGVGLLLAAACLH 206
DB 121 RQNFRCLELQCPDPSSTLPWPSPRPLEATAPAPQPLLLLLLPGVGLLLAAACLH 180
QY 207 WQTRRRTPRPGQVPPVPSPODLLVEH 235
DB 181 WQTRRRTPRPGQVPPVPSPODLLVEH 209

DB 181 WQTRRRTPRPGQVPPVPSPODLLVEH 209

RESULT 15

US-09-109-100-8
Sequence 8, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 209
TYPE: PRT
ORGANISM: Homo sapiens
US-09-109-100-8

Query Match 89.0%; Score 1106; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 7.6e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLDYPYTVASNLQDEELCGGLMRVLVAQRMERL 86
DB 1 TQDCSFQHSPISSDFAVKIRELSYLLDYPYTVASNLQDEELCGGLMRVLVAQRMERL 60
QY 87 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 146
DB 61 KTVAGSKMOGLLERVNTIEHFVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPWIT 120
QY 147 RQNFRCLELQCPDPSSTLPWPSPRPLEATAPAPQPLLLLLLPGVGLLLAAACLH 206
DB 121 RQNFRCLELQCPDPSSTLPWPSPRPLEATAPAPQPLLLLLLPGVGLLLAAACLH 180
QY 207 WQTRRRTPRPGQVPPVPSPODLLVEH 235
DB 181 WQTRRRTPRPGQVPPVPSPODLLVEH 209

Search completed: May 27, 2003, 18:28:59
Job time: 17 secs